GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 30, 2003, 15:59:39 ; Search time 69 Seconds
(without alignments)
42.486 Million cell updates/sec

Title: US-09-904-753-4
Perfect score: 109
Sequence: 1 GIGKFLKKAKKFGKAFVKILKK 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	109	100.0	22	14	AAR35389	Amphiphilic peptid
2	109	100.0	22	15	AAR50450	Amphiphilic peptid
3	109	100.0	22	15	AAR56958	Peptide which neut
4	109	100.0	22	15	AAR54895	Ion channel formin
5	109	100.0	22	17	AAR99103	Magainin-derived a
6	109	100.0	22	17	AAR99119	Magainin-derived a
7	109	100.0	22	17	AAR92826	Amphiphilic peptid
8	109	100.0	22	17	AAR92818	Amphiphilic peptid
9	109	100.0	22	19	AAW66287	Magainin II analog
10	109	100.0	22	19	AAW66505	Amphiphilic peptid
11	109	100.0	22	19	AAW66303	Magainin II analog
12	109	100.0	22	20	AAY22253	Magainin II peptid
13	109	100.0	22	20	AAY10793	Peptide used to ma
14	109	100.0	22	20	AAW87610	Antimicrobial pept
15	109	100.0	22	20	AAW87602	Antimicrobial pept
16	109	100.0	22	21	AAY69907	Peptide MSI-344.
17	109	100.0	22	21	AAY69909	Peptide MSI-78. S
18	109	100.0	22	21	AAY44327	Antimicrobial pept
19	109	100.0	22	22	AAG65532	Magainin-2 derived
20	109	100.0	22	23	ABB81264	Pexiganan antibact
21	109	100.0	22	23	AAE22506	Biologically activ
22	109	100.0	23	15	AAR50451	Amphiphilic peptid
23	109	100.0	23	15	AAR54888	Ion channel formin
24	109	100.0	23	15	AAR54889	Ion channel formin
25	109	100.0	23	15	AAR54890	Ion channel formin
26	109	100.0	23	15	AAR54891	Ion channel formin
27	109	100.0	23	19	AAW66493	Amphiphilic peptid
28	109	100.0	23	19	AAW66494	Amphiphilic peptid
29	109	100.0	23	19	AAW66495	Amphiphilic peptid
30	109	100.0	23	21	AAY44326	Antimicrobial pept
31	109	100.0	24	15	AAR54892	Ion channel formin
32	109	100.0	24	15	AAR54896	Ion channel formin
33	109	100.0	24	19	AAW66496	Amphiphilic peptid
34	109	100.0	25	15	AAR54893	Ion channel formin
35	109	100.0	25	15	AAR54894	Ion channel formin
36	109	100.0	25	15	AAR54897	Ion channel formin
37	109	100.0	25	19	AAW66497	Amphiphilic peptid
38	109	100.0	25	19	AAW66498	Amphiphilic peptid
39	109	100.0	26	15	AAR54898	Ion channel formin
40	109	100.0	26	19	AAW66499	Amphiphilic peptid
41	109	100.0	28	21	ABB08598	Peptide antibiotic
42	109	100.0	36	21	AAY69910	Peptide MSI-1850.
43	109	100.0	67	21	AAY69908	Peptide MSI-1922.
44	109	100.0	84	20	AAW87599	Guamerin/MSI-78 fu
45	109	100.0	84	20	AAW87600	Guamerin/MSI-78 fu

ALIGNMENTS

RESULT 1
AAR35389
ID AAR35389 standard; peptide; 22 AA.
XX
AC AAR35389;
XX
DT 07-JUN-1993 (first entry)
XX
DE Amphiphilic peptide #120 used to treat oral infections.
XX
KW Adverse oral conditions; amphipathic; anti-bacterial; anti-viral;
KW anti-fungal; dental plaque; dental caries; periodontal disease;
KW gingivitis; ionophore; ion-channel forming.
XX
OS Synthetic.
XX
PN WO9301723-A.
XX
PD 04-FEB-1993.
XX
PF 09-JUL-1992; 92WO-US05757.
XX
PR 25-JUL-1991; 91US-0735070.
XX
PA (MAGA-) MAGAININ PHARM INC.
XX
PI Berkowitz B, Jacob L;
XX
DR WPI; 1993-058434/07.
XX
PT Peptide(s) for prophylaxis and treatment of oral disorders - used
PT for periodontal disease, plaque, dental caries, gingivitis, etc.
XX

PS Example 5; Page 134; 143pp; English.
XX
CC This is a preferred amphiphilic peptide for use in preventing or
CC treating adverse oral conditions. The peptide is an ionophore (i.e.
CC an ion-channel forming peptide) which has anti-bacterial, anti-viral,
CC anti-fungal activity, etc. making it suitable for use in oral
CC compositions to treat or prevent periodontal disease, plaque, dental
CC caries, halitosis and gingivitis. The anti-bacterial action will also
CC be useful against bacteria associated with dental implant infections
CC and the peptides can stimulate the healing of wounds in the oral
CC cavity. The minimum inhibitory concn. (microg/ml) for peptide #120
CC was determined on various oral bacteria. For example, against
CC Enterobacter cloacae (which is similar to most of the Gram-negative
CC organisms associated with periimplantitis), the peptide had an MIC
CC of 8, c.f. an MIC of 128 microg/ml against E.cloacae for
CC chlorhexidine gluconate which is commonly used in a rinse after
CC denture implant surgery.
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 109; DB 14; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIGKFLKKAKKFGKAFVKILKK 22
||||||||||||||||||||||
Db 1 GIGKFLKKAKKFGKAFVKILKK 22

RESULT 2
AAR50450
ID AAR50450 standard; peptide; 22 AA.
XX
AC AAR50450;
XX
DT 17-OCT-1994 (first entry)
XX
DE Amphiphilic peptide #115.
XX
KW Amphiphilic peptide; aprotic organic solvent; alcohol; antitumour;
KW antibiotic; antimicrobial; antifungal; antiparasitic; anticancer;
KW antiviral; human; animal; plant; ion-channel; forming peptide.
XX
OS Synthetic.
XX
PN WO9405308-A.
XX
PD 17-MAR-1994.
XX
PF 13-AUG-1993; 93WO-US07694.
XX
PR 28-AUG-1992; 92US-0936504.
XX
PA (MAGA-) MAGAININ PHARM INC.
XX
PI Williams JI;
XX
DR WPI; 1994-100846/12.
XX
PT Purifying amphiphilic protein or peptide by solvent extn. -
PT partic. for recombinant, ion-channel forming peptide(s) such as
PT magainins, avoids use of chaotropic agents.
XX
PS Disclosure; Page 125; 135pp; English.
XX
CC The sequences given in AAR50336-451 are amphiphilic peptides which
CC were isolated by the method of the invention. A material containing
CC amphiphilic peptides such as these, was treated with a mixt. of
CC aprotic organic solvent and alcohol to form a single miscible
CC solution. This solution was then treated with a aqueous solution to
CC form an aqueous phase solution containing the peptides and an
CC organic solvent phase, and the peptides were isolated from the
CC aqueous phase. The isolated peptides may be useful as antibiotic,
CC antimicrobial, antifungal, antiparasitic, antitumour, anticancer,
CC and/or antiviral agents for treatment of humans, animals or plants.
CC These peptides are esp. ion-channel forming peptides which enable
CC biologically active ions to enter cells.
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 109; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIGKFLKKAKKFGKAFVKILKK 22
||||||||||||||||||||||
Db 1 GIGKFLKKAKKFGKAFVKILKK 22

RESULT 3
AAR56958
ID AAR56958 standard; peptide; 22 AA.
XX
AC AAR56958;
XX
DT 17-MAR-1995 (first entry)
XX
DE Peptide which neutralises bacterial endotoxin.
XX
KW septic shock; bacterial endotoxin; lipopolysaccharide; LPS;
KW gram negative bacteria; conjugate moiety; septicemia; neutralising;
KW longer activity; polyvinylpyrrolidone; dextran; hetastarch;
KW polyvinyl alcohol; ion-channel forming; amphiphilic.
XX
OS Synthetic.
XX
PN WO9413697-A.
XX
PD 23-JUN-1994.
XX
PF 06-DEC-1993; 93WO-US11841.
XX
PR 07-DEC-1992; 92US-0987443.
XX
PA (MAGA-) MAGAININ PHARM INC.
XX
PI Hendi M, Rao M, Williams TJ;
XX
DR WPI; 1994-217804/26.
XX
PT New conjugates of bioactive amphiphilic peptide(s) and conjugate
PT moiety - are useful for treatment of septic shock
XX
PS Disclosure; Page 120; 141pp; English.
XX
CC Septic shock is often due to the body's reaction to foreign
CC lipopolysaccharide (LPS). The compounds of the invention neutralise
CC bacterial endotoxins without neutralising essential proteins in the
CC plasma of patients, eg.heparins. They also have longer duration of
CC activity than unconjugated peptides. In general peptides such as this
CC are ion-channel forming peptides.The compounds are biologically active
CC peptides linked to a conjugate moiety, eg. carbohydrates, proteins,
CC polyvinylpyrrolidone, polyalkylene glycols and polyvinyl alcohols.
CC The conjugate moiety may be linked at the C- or N-terminal or
CC internally of the peptide. AAR55591-631 and AAR56879-957 are examples
CC of these peptide-conjugate moiety compounds
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 109; DB 15; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIGKFLKKAKKFGKAFVKILKK 22
||||||||||||||||||||||
Db 1 GIGKFLKKAKKFGKAFVKILKK 22

```
RESULT 4
AAR54895
ID   AAR54895 standard; peptide; 22 AA.
XX
AC   AAR54895;
XX
DT   03-NOV-1994  (first entry)
XX
DE   Ion channel forming amphiphilic peptide.
XX
KW   Ionophore; antimicrobial; antiviral; antibacterial; antiparasitic;
KW   spermicide; wound healing; burns; anticancer; preservative;
KW   sterilant; disinfectant; plant protection.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   15
FT                   /note= "could be in D form"
FT   Modified-site   21
FT                   /note= "could be in D form"
FT   Modified-site   22
FT                   /note= "could be in D form"
XX
PN   WO9409810-A.
XX
PD   11-MAY-1994.
XX
PF   22-OCT-1993;   93WO-US10337.
XX
PR   26-OCT-1992;   92US-0965663.
XX
PA   (MAGA-) MAGAININ PHARM INC.
XX
PI   Kari UP,  Maloy WL;
XX
DR   WPI; 1994-167120/20.
XX
PT   New ion channel forming amphiphilic - useful as antimicrobial,
PT   antitumour, antiparasitic and spermicidal agents
XX
PS   Claim 19; Page 39; 43pp; English.
XX
CC   The peptide sequence is that of an ion forming peptide used
CC   to inhibit the growth of target cells, viruses and virally infected
CC   cells in a host, i.e. they are antimicrobial, antiviral,
CC   antibacterial, anticancer and antiparasitic agents or spermicides.
CC   They can also be used to stimulate wound healing and can be used to
CC   treat burns.  The peptides can be used in human or veterinary
CC   medicine as preservatives, sterilants or disinfectants and in plant
CC   protection.
CC   See also AAR54880-906.
XX
SQ   Sequence   22 AA;

  Query Match            100.0%;  Score 109;  DB 15;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-08;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFVKILKK 22
              ||||||||||||||||||||||
Db          1 GIGKFLKKAKKFGKAFVKILKK 22


RESULT 5
AAR99103
ID   AAR99103 standard; peptide; 22 AA.
XX
AC   AAR99103;
XX
DT   28-OCT-1996  (first entry)
XX
DE   Magainin-derived antimicrobial STD-inhibiting peptide, MSI-78.
XX
KW   STD; sexually transmitted disease; HIV; human immunodeficiency virus;
KW   herpes simplex virus; HSV; Neisseria gonnorhoeae; Candida; Chlamydia;
KW   magainin; antimicrobial; squalamine.
XX
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   22
FT                   /note= "amidated"
XX
PN   WO9608270-A2.
XX
PD   21-MAR-1996.
XX
PF   13-SEP-1995;   95WO-US11675.
XX
PR   13-SEP-1994;   94US-0305475.
XX
PA   (MAGA-) MAGAININ PHARM INC.
XX
PI   Bedi G,  Jacob L,  Williams T,  Zasloff M;
XX
DR   WPI; 1996-179725/18.
XX
PT   Inhibiting sexually transmitted disease e.g. HIV or herpes simplex -
PT   by administering magainin antimicrobial or squalamine cpd. to
PT   inhibit transmission
XX
PS   Disclosure; Page 16; 60pp; English.
XX
CC   AAR99095-R99107 are antimicrobial, magainin-analogue peptides that may
CC   be used to treat sexually transmitted diseases (STDs) caused by
CC   Chlamydia, HIV, herpes simplex virus, Neisseria gonnorhoeae or
CC   Candida infection. The peptides inhibit STDs by either killing the
CC   infectious organism, impeding the infection mechanism or
CC   interrupting the replication cycle of the organism. Squalamine (an
CC   aminosterol host defence molecule of the dog fish shark Squalus
CC   acanthias) and PGLa (a frog antimicrobial peptide) analogues may
CC   also be useful in inhibiting STD infection and transmission.
XX
SQ   Sequence   22 AA;

  Query Match            100.0%;  Score 109;  DB 17;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-08;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFVKILKK 22
              ||||||||||||||||||||||
Db          1 GIGKFLKKAKKFGKAFVKILKK 22


RESULT 6
AAR99119
ID   AAR99119 standard; peptide; 22 AA.
XX
AC   AAR99119;
XX
DT   28-OCT-1996  (first entry)
XX
DE   Magainin-derived antimicrobial STD-inhibiting peptide, MSI-344.
XX
KW   STD; sexually transmitted disease; HIV; human immunodeficiency virus;
KW   herpes simplex virus; HSV; Neisseria gonnorhoeae; Candida; Chlamydia;
KW   magainin; antimicrobial; squalamine.
XX
OS   Synthetic.
XX
PN   WO9608270-A2.
XX
PD   21-MAR-1996.
```

XX
PF 13-SEP-1995; 95WO-US11675.
XX
PR 13-SEP-1994; 94US-0305475.
XX
PA (MAGA-) MAGAININ PHARM INC.
XX
PI Bedi G, Jacob L, Williams T, Zasloff M;
XX
DR WPI; 1996-179725/18.
XX
PT Inhibiting sexually transmitted disease e.g. HIV or herpes simplex -
PT by administering magainin antimicrobial or squalamine cpd. to
PT inhibit transmission
XX
PS Example 1; Page 32; 60pp; English.
XX
CC AAR99116-R99123 are antimicrobial, magainin-analogue peptides that may
CC be used to treat sexually transmitted diseases (STDs) caused by
CC Chlamydia, HIV, herpes simplex virus, Neisseria gonnorhoeae or
CC Candida infection. The peptides inhibit STDs by either killing the
CC infectious organism, impeding the infection mechanism or
CC interrupting the replication cycle of the organism. Squalamine (an
CC aminosterol host defence molecule of the dog fish shark Squalus
CC acanthias) and PGLa (a frog antimicrobial peptide) analogues may
CC also be useful in inhibiting STD infection and transmission.
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 109; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIGKFLKKAKKFGKAFVKILKK 22
||||||||||||||||||||||
Db 1 GIGKFLKKAKKFGKAFVKILKK 22

RESULT 7
AAR92826
ID AAR92826 standard; Peptide; 22 AA.
XX
AC AAR92826;
XX
DT 24-SEP-1996 (first entry)
XX
DE Amphiphilic peptide MSI-78.
XX
KW MSI-78; amphiphilic peptide; recombinant production;
KW protease deficient; microbial host cell; expression vector;
KW Escherichia coli; K-12 cell; vector; cleavable fusion protein;
KW carbohydrate binding protein; anti-parasitic; anti-fungal;
KW anti-tumour; anti-cancer; anti-viral; anti-microbial.
XX
OS Synthetic.
XX
PN WO9604373-A2.
XX
PD 15-FEB-1996.
XX
PF 26-JUL-1995; 95WO-US10219.
XX
PR 29-JUL-1994; 94US-0282030.
XX
PA (MAGA-) MAGAININ PHARM INC.
XX
PI Anderson GM, Kari P, Pierce JC, Williams JI;
XX
DR WPI; 1996-129390/13.
XX
PT Recombinant production of amphiphilic peptide in protease deficient
PT microbial host, pref. E. coli K-12 - useful in prodn. of
PT antimicrobial, antiviral and anticancer peptide(s)
XX
PS Example 12; Page 67; 103pp; English.
XX
CC A DNA encoding the present sequence, MSI-78 (an amphiphilic
CC peptide) can be used in 2 novel methods for the recombinant prodn.
CC of MSI-78. The 1st method comprises transforming a protease
CC deficient (PD) microbial host cell with an expression vector contg.
CC the DNA, under the control of a regulatory sequence operable in the
CC host, and expressing the peptide in the transformed host. The 2nd
CC method comprises transforming an E. coli PD K-12 cell with a vector
CC that expresses a cleavable fusion protein, comprising at least part
CC of a carbohydrate binding protein (CBP) and the peptide, expressing
CC the fusion protein in the cell and cleaving the protein to obtain
CC the peptide substantially free of CBP residues. These methods for
CC producing and processing MSI-78 allow high levels of the
CC peptide to accumulate in certain PD microbial host cells, despite
CC the peptides anti-microbial potency, and efficient recovery of the
CC full length peptide. The peptide produced, unlike most natural
CC analogous peptides, exhibits a broader range of activity and/or
CC greater potency compared to a related natural peptide, e.g. the
CC peptide may be used as an anti-parasitic, anti-fungal, anti-tumour,
CC anti-cancer or an anti-viral agent.
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 109; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIGKFLKKAKKFGKAFVKILKK 22
||||||||||||||||||||||
Db 1 GIGKFLKKAKKFGKAFVKILKK 22

RESULT 8
AAR92818
ID AAR92818 standard; Peptide; 22 AA.
XX
AC AAR92818;
XX
DT 23-SEP-1996 (first entry)
XX
DE Amphiphilic peptide MSI-344.
XX
KW MSI-344; amphiphilic peptide; recombinant production;
KW protease deficient; microbial host cell; expression vector;
KW Escherichia coli; K-12 cell; vector; cleavable fusion protein;
KW carbohydrate binding protein; anti-parasitic; anti-fungal;
KW anti-tumour; anti-cancer; anti-viral; anti-microbial.
XX
OS Synthetic.
XX
PN WO9604373-A2.
XX
PD 15-FEB-1996.
XX
PF 26-JUL-1995; 95WO-US10219.
XX
PR 29-JUL-1994; 94US-0282030.
XX
PA (MAGA-) MAGAININ PHARM INC.
XX
PI Anderson GM, Kari P, Pierce JC, Williams JI;
XX
DR WPI; 1996-129390/13.
DR N-PSDB; AAT17893.
XX
PT Recombinant production of amphiphilic peptide in protease deficient
PT microbial host, pref. E. coli K-12 - useful in prodn. of
PT antimicrobial, antiviral and anticancer peptide(s)
XX
PS Claim 6; Page 16; 103pp; English.
XX

CC The DNA encoding the present sequence, MSI-344 (an amphiphilic
CC peptide) is used in 2 novel methods for the recombinant prodn. of
CC MSI-344. The 1st method comprises transforming a protease
CC deficient (PD) microbial host cell with an expression vector contg.
CC the DNA, under the control of a regulatory sequence operable in the
CC host, and expressing the peptide in the transformed host. The 2nd
CC method comprises transforming an E. coli PD K-12 cell with a vector
CC that expresses a cleavable fusion protein, comprising at least part
CC of a carbohydrate binding protein (CBP) and the peptide, expressing
CC the fusion protein in the cell and cleaving the protein to obtain
CC the peptide substantially free of CBP residues. These methods for
CC producing and processing MSI-344 allow high levels of the
CC peptide to accumulate in certain PD microbial host cells, despite
CC the peptides anti-microbial potency, and efficient recovery of the
CC full length peptide. The peptide produced, unlike most natural
CC analogous peptides, exhibits a broader range of activity and/or
CC greater potency compared to a related natural peptide, e.g. the
CC peptide may be used as an anti-parasitic, anti-fungal, anti-tumour,
CC anti-cancer or an anti-viral agent.
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 109; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIGKFLKKAKKFGKAFVKILKK 22
||||||||||||||||||||||
Db 1 GIGKFLKKAKKFGKAFVKILKK 22

RESULT 9
AAW66287
ID AAW66287 standard; peptide; 22 AA.
XX
AC AAW66287;
XX
DT 25-NOV-1998 (first entry)
XX
DE Magainin II analogue containing D-amino acids.
XX
KW magainin; analogue; antimicrobial; antitumour; wound healing.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1..22
FT /note= "each amino acid residue which is not a Gly
FT residue is a D-amino acid residue"
XX
PN US5792831-A.
XX
PD 11-AUG-1998.
XX
PF 17-NOV-1994; 94US-0343882.
XX
PR 05-OCT-1993; 93US-0133740.
PR 08-FEB-1990; 90US-0476629.
PR 14-MAY-1990; 90US-0522688.
PR 28-APR-1992; 92US-0874685.
PR 17-NOV-1994; 94US-0343882.
XX
PA (MAGA-) MAGAININ PHARM INC.
XX
PI Maloy WL;
XX
DR WPI; 1998-456190/39.
XX
PT Magainin peptide analogues - useful as antimicrobial or antitumour
PT agents, etc.
XX
PS Claim 2; Column 44; 25pp; English.
XX

514 912

CC The invention relates to analogues of a magainin I peptide of formula:
CC GIGKFLHSAGKFGKAFVGEIMKS or a magainin II peptide of formula:
CC GIGKFLHSAKKFGKAFVGEIMNS, where all amino acids other than Gly are D-amino
CC acids and the analogues are in carboxy- or amide-terminated form. In the
CC analogues, the amino acid at position 19 is deleted and at least one
CC amino acid in the following positions is substituted as follows: 3:
CC D-Leu; 7: D-Lys; 8: D-Lys or D-Ala; 10: D-Ala or D-Lys; 13: D-Trp, D-Leu,
CC D-Phe or D-Ala; 15: D-Phe; 16: D-Ala; 18: D-Lys, D-Ala or D-Phe; 21:
CC D-Lys, D-Ile or D-Leu; 22: D-Lys; 23: D-Lys, D-Ser or D-Asn.
CC Magainin I or II analogues or related peptides may be used as
CC antimicrobial agents, antiviral agents, antibiotics, antitumour agents,
CC antiparasitic agents, spermicides, preservatives or sterilants, or agents
CC for promoting wound healing. The present sequence represents a
CC specifically claimed magainin II analogue.
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 109; DB 19; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIGKFLKKAKKFGKAFVKILKK 22
||||||||||||||||||||||
Db 1 GIGKFLKKAKKFGKAFVKILKK 22

RESULT 10
AAW66505
ID AAW66505 standard; peptide; 22 AA.
XX
AC AAW66505;
XX
DT 25-NOV-1998 (first entry)
XX
DE Amphiphilic peptide.
XX
KW magainin; analogue; antimicrobial; antitumour; wound healing;
KW CPF; amphiphilic; XPF peptide.
XX
OS Synthetic.
XX
PN US5792831-A.
XX
PD 11-AUG-1998.
XX
PF 17-NOV-1994; 94US-0343882.
XX
PR 05-OCT-1993; 93US-0133740.
PR 08-FEB-1990; 90US-0476629.
PR 14-MAY-1990; 90US-0522688.
PR 28-APR-1992; 92US-0874685.
PR 17-NOV-1994; 94US-0343882.
XX
PA (MAGA-) MAGAININ PHARM INC.
XX
PI Maloy WL;
XX
DR WPI; 1998-456190/39.
XX
PT Magainin peptide analogues - useful as antimicrobial or antitumour
PT agents, etc.
XX
PS Disclosure; Column 24; 25pp; English.
XX
CC The invention relates to analogues of a magainin I or II, D-form
CC analogues, deletion analogues or related peptides. It also relates
CC to basic polypeptides having at least 16 amino acids, including at least
CC 8 hydrophobic amino acids and at least 8 hydrophilic amino acids. The
CC peptides may be used as antimicrobial agents, antiviral agents,
CC antibiotics, antitumour agents, antiparasitic agents, spermicides,
CC preservatives or sterilants, or agents for promoting wound healing. The
CC present sequence represents a specific example of a peptide disclosed in
CC the specification.

```
XX
SQ   Sequence   22 AA;

  Query Match            100.0%;  Score 109;  DB 19;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-08;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFVKILKK 22
              ||||||||||||||||||||||
Db          1 GIGKFLKKAKKFGKAFVKILKK 22


RESULT 11
AAW66303
ID   AAW66303 standard; peptide; 22 AA.
XX
AC   AAW66303;
XX
DT   25-NOV-1998  (first entry)
XX
DE   Magainin II analogue.
XX
KW   magainin; analogue; antimicrobial; antitumour; wound healing.
XX
OS   Synthetic.
XX
PN   US5792831-A.
XX
PD   11-AUG-1998.
XX
PF   17-NOV-1994;   94US-0343882.
XX
PR   05-OCT-1993;   93US-0133740.
PR   08-FEB-1990;   90US-0476629.
PR   14-MAY-1990;   90US-0522688.
PR   28-APR-1992;   92US-0874685.
PR   17-NOV-1994;   94US-0343882.
XX
PA   (MAGA-) MAGAININ PHARM INC.
XX
PI   Maloy WL;
XX
DR   WPI; 1998-456190/39.
XX
PT   Magainin peptide analogues - useful as antimicrobial or antitumour
PT   agents, etc.
XX
PS   Disclosure; Column 5; 25pp; English.
XX
CC   The invention relates to analogues of a magainin I peptide of formula:
CC   GIGKFLHSAGKFGKAFVGEIMKS or a magainin II peptide of formula:
CC   GIGKFLHSAKKFGKAFVGEIMNS. Magainin I or II analogues or related peptides
CC   may be used as antimicrobial agents, antiviral agents, antibiotics,
CC   antitumour agents, antiparasitic agents, spermicides, preservatives or
CC   sterilants, or agents for promoting wound healing. The present sequence
CC   represents a magainin II analogue.
XX
SQ   Sequence   22 AA;

  Query Match            100.0%;  Score 109;  DB 19;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-08;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFVKILKK 22
              ||||||||||||||||||||||
Db          1 GIGKFLKKAKKFGKAFVKILKK 22


RESULT 12
AAY22253
ID   AAY22253 standard; peptide; 22 AA.
XX
AC   AAY22253;
XX
DT   20-SEP-1999  (first entry)
XX
DE   Magainin II peptide analogue.
XX
KW   Magainin I; magainin II; proliferation inhibitor; microbe inhibitor;
KW   tumour growth inhibitor; antibacterial agent.
XX
OS   Mammalia.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Modified-site   22
FT                   /note= "amidated"
XX
PN   US5912231-A.
XX
PD   15-JUN-1999.
XX
PF   14-NOV-1994;   94US-0338882.
XX
PR   15-NOV-1990;   90US-0615125.
PR   07-JUL-1989;   89US-0376754.
PR   14-NOV-1994;   94US-0338882.
XX
PA   (SCRI ) SCRIPPS CLINIC & RES FOUND.
XX
PI   Cuervo JH,  Houghten RA;
XX
DR   WPI; 1999-428521/36.
XX
PT   Analogues of Magainin peptides useful for inhibiting tumour growth
PT   and microbial proliferation
XX
PS   Claim 14; Column 55; 30pp; English.
XX
CC   This sequence represents a Magainin analogue of the invention. The
CC   invention relates to analogues of Magainin I and Magainin II. The
CC   peptides are useful for inhibiting the proliferation of microbes,
CC   especially bacteria and for inhibiting the growth of tumours.
CC   Compositions for use as antibacterial agents are used at a concentration
CC   of 0.5-5 %.
XX
SQ   Sequence   22 AA;

  Query Match            100.0%;  Score 109;  DB 20;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 2.1e-08;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFVKILKK 22
              ||||||||||||||||||||||
Db          1 GIGKFLKKAKKFGKAFVKILKK 22


RESULT 13
AAY10793
ID   AAY10793 standard; peptide; 22 AA.
XX
AC   AAY10793;
XX
DT   11-MAY-1999  (first entry)
XX
DE   Peptide used to make biologically active peptides.
XX
KW   Sepsis; septic shock; Pseudomonas aeruginosa; cystic fibrosis;
KW   antimicrobial; antiviral; antibacterial; antifungal; antitumour;
KW   antiparasitic; spermicide; preservative; sterilant; disinfectant;
KW   wound healing; burn; skin infection; eye infection; solid tumour;
KW   leukaemia; non-small cell lung cancer; adenocarcinoma; plant infection;
KW   periodontal disease; plaque; gingivitis; caries; Streptococcus mutans.
XX
OS   Synthetic.
XX
```

PN WO9903488-A2.
XX
PD 28-JAN-1999.
XX
PF 15-JUL-1998; 98WO-US14610.
XX
PR 15-JUL-1997; 97US-0893006.
XX
PA (MAGA-) MAGAININ PHARM INC.
XX
PI Kari UP, McLane M, Williams TJ;
XX
DR WPI; 1999-131859/11.
XX
PT Treating sepsis or septic shock with N-modified ion-channel forming
PT peptide - or its methane sulphonate derivative of reduced toxicity,
PT also generally useful as antimicrobial and antitumour agents
XX
PS Example 7; Page 201; 202pp; English.
XX
CC AAY10640-795 represent peptides used in the production of biologically
CC active peptides with reduced toxicity. The biologically active peptides
CC are used to treat sepsis or septic shock, and comprise the formula:
CC T-N(W)-X, where X = biologically active, amphipathic, ion-channel
CC forming peptide or protein; T = lipophilic group; and W = hydrogen or T.
CC The peptides are particularly used to treat infections by Pseudomonas
CC aeruginosa in patients with cystic fibrosis, but more generally as
CC anti-microbial, antiviral, antibacterial, antifungal, antitumour or
CC antiparasitic agents, and also as spermicides, e.g. as preservatives,
CC sterilants, and disinfectants in human and veterinary medicine. They
CC can be used to stimulate wound healing, treat burns and/or skin and
CC burn infections, eye infections, solid tumours or leukaemia
CC (particularly non-small cell lung cancer and adenocarcinoma, including
CC those resistant to other antitumour agents), and also for treatment of
CC infections in plants, and, when formulated in oral hygiene formulations,
CC for treating or preventing periodontal disease, plaque, gingivitis and/or
CC caries (specifically by action on Streptococcus mutans).
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 109; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIGKFLKKAKKFGKAFVKILKK 22
||||||||||||||||||||||
Db 1 GIGKFLKKAKKFGKAFVKILKK 22

RESULT 14
AAW87610
ID AAW87610 standard; peptide; 22 AA.
XX
AC AAW87610;
XX
DT 19-MAR-1999 (first entry)
XX
DE Antimicrobial peptide Magainin (MSI-344).
XX
KW Antimicrobial; fusion; acidic peptide; recombinant; microorganism;
KW guamerin; basic peptide; Magainin.
XX
OS Rana sp.
XX
PN WO9854336-A1.
XX
PD 03-DEC-1998.
XX
PF 28-MAY-1998; 98WO-KR00132.
XX
PR 09-APR-1998; 98KR-0013372.
PR 28-MAY-1997; 97KR-0021312.
XX
PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
PA (SAMY-) SAMYANG GENEX CORP.
XX
PI Hong S, Kang MH, Kim JH, Kim S, Lee H, Lee JH;
XX
DR WPI; 1999-059844/05.
DR N-PSDB; AAV83789.
XX
PT New method for mass production of antimicrobial peptides - by
PT constructing fusion genes comprising acidic and antimicrobial
PT peptide genes and transforming host with vector containing these
XX
PS Example 6; Page 18; 52pp; English.
XX
CC The invention relates to mass production of antimicrobial peptides. The
CC method comprises constructing a fusion gene containing a first gene
CC encoding a negatively charged acidic peptide having at least two cysteine
CC residues, and a second gene encoding a positively charged basic
CC antimicrobial peptide. A host microorganism is transformed with a vector
CC containing the fusion gene and then cultured. The expressed antimicrobial
CC peptide is then recovered. The method is used to mass produce
CC antimicrobial peptides in recombinant microorganisms. The inhibitory
CC effect of the expressed antimicrobial peptide upon the growth of the host
CC microorganism is considerably reduced by fusing it to the acidic peptide.
CC Therefore, the use of the fusion gene provides an economic, recombinant
CC alternative of mass producing antimicrobial peptides, which overcomes the
CC disadvantages of low-productivity and poor economy, previously
CC encountered by recombinant and chemical methods. The present sequence
CC represents an antimicrobial peptide Magainin. The encoding DNA sequence
CC can be used along with the acidic peptide Guamerin gene in the
CC construction of the fusion gene.
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 109; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIGKFLKKAKKFGKAFVKILKK 22
||||||||||||||||||||||
Db 1 GIGKFLKKAKKFGKAFVKILKK 22

RESULT 15
AAW87602
ID AAW87602 standard; peptide; 22 AA.
XX
AC AAW87602;
XX
DT 19-MAR-1999 (first entry)
XX
DE Antimicrobial peptide MSI-78 peptide fragment.
XX
KW Antimicrobial; fusion; acidic peptide; recombinant; microorganism;
KW basic peptide; Buforin II.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FT Modified-site 22
FT /note= "C-terminal amide"
XX
PN WO9854336-A1.
XX
PD 03-DEC-1998.
XX
PF 28-MAY-1998; 98WO-KR00132.
XX
PR 09-APR-1998; 98KR-0013372.
PR 28-MAY-1997; 97KR-0021312.
XX
PA (KOAD) KOREA ADV INST SCI & TECHNOLOGY.
PA (SAMY-) SAMYANG GENEX CORP.

XX
PI Hong S, Kang MH, Kim JH, Kim S, Lee H, Lee JH;
XX
DR WPI; 1999-059844/05.
XX
PT New method for mass production of antimicrobial peptides - by
PT constructing fusion genes comprising acidic and antimicrobial
PT peptide genes and transforming host with vector containing these
XX
PS Example 4; Page 14; 52pp; English.
XX
CC The invention relates to mass production of antimicrobial peptides. The
CC method comprises constructing a fusion gene containing a first gene
CC encoding a negatively charged acidic peptide having at least two cysteine
CC residues, and a second gene encoding a positively charged basic
CC antimicrobial peptide. A host microorganism is transformed with a vector
CC containing the fusion gene and then cultured. The expressed antimicrobial
CC peptide is then recovered. The method is used to mass produce
CC antimicrobial peptides in recombinant microorganisms. The inhibitory
CC effect of the expressed antimicrobial peptide upon the growth of the host
CC microorganism is considerably reduced by fusing it to the acidic peptide.
CC Therefore, the use of the fusion gene provides an economic, recombinant
CC alternative of mass producing antimicrobial peptides, which overcomes the
CC disadvantages of low-productivity and poor economy, previously
CC encountered by recombinant and chemical methods. The present sequence
CC represents a fragment of the MSI-78 antimicrobial peptide.
XX
SQ Sequence 22 AA;

Query Match 100.0%; Score 109; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 2.1e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GIGKFLKKAKKFGKAFVKILKK 22
              ||||||||||||||||||||||
Db          1 GIGKFLKKAKKFGKAFVKILKK 22
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Search completed: June 30, 2003, 16:07:38
Job time : 70 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 30, 2003, 16:06:25 ; Search time 26 Seconds
(without alignments)
24.896 Million cell updates/sec

Title: US-09-904-753-4
Perfect score: 109
Sequence: 1 GIGKFLKKAKKFGKAFVKILKK 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	109	100.0	22	1	US-08-282-030-4	Sequence 4, Appli
2	109	100.0	22	1	US-08-343-882-2	Sequence 2, Appli
3	109	100.0	22	4	US-09-230-180-14	Sequence 14, Appl
4	109	100.0	22	4	US-09-230-180-32	Sequence 32, Appl
5	109	100.0	22	4	US-09-115-737-154	Sequence 154, App
6	109	100.0	22	5	PCT-US95-10219-4	Sequence 4, Appli
7	109	100.0	23	1	US-07-965-663A-8	Sequence 8, Appli
8	109	100.0	23	1	US-07-965-663A-9	Sequence 9, Appli
9	109	100.0	23	1	US-07-965-663A-10	Sequence 10, Appl
10	109	100.0	23	1	US-07-965-663A-11	Sequence 11, Appl
11	109	100.0	24	1	US-07-965-663A-12	Sequence 12, Appl
12	109	100.0	25	1	US-07-965-663A-13	Sequence 13, Appl
13	109	100.0	25	1	US-07-965-663A-14	Sequence 14, Appl
14	109	100.0	26	1	US-07-965-663A-15	Sequence 15, Appl
15	109	100.0	84	4	US-09-230-180-7	Sequence 7, Appli
16	109	100.0	84	4	US-09-230-180-8	Sequence 8, Appli
17	108	99.1	22	1	US-07-965-663A-19	Sequence 19, Appl
18	107	98.2	22	1	US-08-343-882-4	Sequence 4, Appli
19	107	98.2	22	4	US-09-115-737-155	Sequence 155, App
20	106	97.2	22	1	US-07-965-663A-6	Sequence 6, Appli
21	104	95.4	22	1	US-07-965-663A-7	Sequence 7, Appli
22	104	95.4	22	1	US-07-965-663A-21	Sequence 21, Appl
23	104	95.4	22	1	US-08-282-030-51	Sequence 51, Appl
24	104	95.4	22	2	US-08-338-882-55	Sequence 55, Appl
25	104	95.4	22	5	PCT-US95-10219-51	Sequence 51, Appl
26	103	94.5	21	1	US-07-965-663A-1	Sequence 1, Appli
27	103	94.5	22	1	US-07-965-663A-20	Sequence 20, Appl
28	103	94.5	23	1	US-07-965-663A-16	Sequence 16, Appl
29	102	93.6	22	2	US-08-338-882-52	Sequence 52, Appl
30	100	91.7	23	1	US-08-282-030-6	Sequence 6, Appli
31	100	91.7	23	5	PCT-US95-10219-6	Sequence 6, Appli
32	99	90.8	21	1	US-07-965-663A-22	Sequence 22, Appl
33	99	90.8	22	2	US-08-338-882-16	Sequence 16, Appl
34	99	90.8	22	2	US-08-338-882-58	Sequence 58, Appl
35	96	88.1	22	2	US-08-338-882-53	Sequence 53, Appl
36	96	88.1	22	2	US-08-338-882-54	Sequence 54, Appl
37	94	86.2	22	1	US-08-434-120-117	Sequence 117, App
38	94	86.2	22	1	US-08-343-882-6	Sequence 6, Appli
39	94	86.2	22	2	US-08-338-882-56	Sequence 56, Appl
40	94	86.2	23	4	US-09-127-680-14	Sequence 14, Appl
41	94	86.2	38	4	US-09-127-680-16	Sequence 16, Appl
42	92	84.4	22	1	US-08-343-882-3	Sequence 3, Appli
43	92	84.4	22	2	US-08-338-882-57	Sequence 57, Appl
44	91	83.5	22	1	US-07-965-663A-4	Sequence 4, Appli
45	91	83.5	22	1	US-08-434-120-115	Sequence 115, App

ALIGNMENTS

RESULT 1
US-08-282-030-4
; Sequence 4, Application US/08282030
; Patent No. 5589364
; GENERAL INFORMATION:
; APPLICANT: Williams, Jon I.
; APPLICANT: Pierce, James C.
; APPLICANT: Anderson, Mark G.
; APPLICANT: Kari, Prasad
; TITLE OF INVENTION: Recombinant Production of Biologically
; TITLE OF INVENTION: Active Peptides and Proteins
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/282,030
; FILING DATE: 29-JUL-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Fordis, Jean B.
; REGISTRATION NUMBER: 32,984
; REFERENCE/DOCKET NUMBER: 05387.0001-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-282-030-4

Query Match 100.0%; Score 109; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 3.4e-08;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIGKFLKKAKKFGKAFVKILKK 22
||||||||||||||||||||||

```
Db          1 GIGKFLKKAKKFGKAFVKILKK 22


RESULT 2
US-08-343-882-2
; Sequence 2, Application US/08343882
; Patent No. 5792831
;  GENERAL INFORMATION:
;    APPLICANT:  Maloy, W. Lee
;    TITLE OF INVENTION:  Compositions of and Treatment
;    TITLE OF INVENTION:  with Biologically Active
;    TITLE OF INVENTION:  Peptides Having D-amino acid
;    TITLE OF INVENTION:  residues
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Carella, Byrne, Bain,
;      ADDRESSEE:  Gilfillan, Cecchi, Stewart &
;      ADDRESSEE:  Olstein
;      STREET:  6 Becker Farm Road
;      CITY:  Roseland
;      STATE:  New Jersey
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 inch diskette
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  DW4.V2
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/343,882
;      FILING DATE:  17-NOV-1994
;      CLASSIFICATION:  514
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/133,740
;      FILING DATE:  05-OCT-1993
;      APPLICATION NUMBER:  07/874,685
;      FILING DATE:  28-APR-1992
;      APPLICATION NUMBER:  07/522,688
;      FILING DATE:  14-MAY-1990
;      APPLICATION NUMBER:  07/476,629
;      FILING DATE:  08-FEB-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Olstein, Elliot M.
;      REGISTRATION NUMBER:  24,025
;      REFERENCE/DOCKET NUMBER:  421250-89
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-343-882-2

  Query Match           100.0%;  Score 109;  DB 1;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 3.4e-08;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFVKILKK 22
              ||||||||||||||||||||||
Db          1 GIGKFLKKAKKFGKAFVKILKK 22


RESULT 3
US-09-230-180-14
; Sequence 14, Application US/09230180
; Patent No. 6183992
; GENERAL INFORMATION:
;  APPLICANT:  Kim, Sun-Chang
;  APPLICANT:  Lee, Jae Hyun
;  APPLICANT:  Kang, Min Hyung
;  APPLICANT:  Kim, Jeong Hyun
;  APPLICANT:  Hong, Seung-Suh
;  APPLICANT:  Lee, Hyun-Soo
;  APPLICANT:  Samyang Genex Corporation
;  APPLICANT:  Korea Advanced Institute of Science and Technology
;  TITLE OF INVENTION:  METHOD FOR MASS PRODUCTION OF
;  TITLE OF INVENTION:  ANTIMICROBIAL PEPTIDE
;  FILE REFERENCE:  6181/0F135
;  CURRENT APPLICATION NUMBER: US/09/230,180
;  CURRENT FILING DATE:  1999-03-10
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00132
;  PRIOR FILING DATE:  1998-05-28
;  PRIOR APPLICATION NUMBER:  KR 13372/1998
;  PRIOR FILING DATE:  1998-04-09
;  PRIOR APPLICATION NUMBER:  KR 21312/1997
;  PRIOR FILING DATE:  1997-05-28.
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 14
;   LENGTH:  22
;   TYPE:  PRT
;   ORGANISM:  Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION:  MSI-78
US-09-230-180-14

  Query Match           100.0%;  Score 109;  DB 4;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 3.4e-08;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFVKILKK 22
              ||||||||||||||||||||||
Db          1 GIGKFLKKAKKFGKAFVKILKK 22


RESULT 4
US-09-230-180-32
; Sequence 32, Application US/09230180
; Patent No. 6183992
; GENERAL INFORMATION:
;  APPLICANT:  Kim, Sun-Chang
;  APPLICANT:  Lee, Jae Hyun
;  APPLICANT:  Kang, Min Hyung
;  APPLICANT:  Kim, Jeong Hyun
;  APPLICANT:  Hong, Seung-Suh
;  APPLICANT:  Lee, Hyun-Soo
;  APPLICANT:  Samyang Genex Corporation
;  APPLICANT:  Korea Advanced Institute of Science and Technology
;  TITLE OF INVENTION:  METHOD FOR MASS PRODUCTION OF
;  TITLE OF INVENTION:  ANTIMICROBIAL PEPTIDE
;  FILE REFERENCE:  6181/0F135
;  CURRENT APPLICATION NUMBER: US/09/230,180
;  CURRENT FILING DATE:  1999-03-10
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00132
;  PRIOR FILING DATE:  1998-05-28
;  PRIOR APPLICATION NUMBER:  KR 13372/1998
;  PRIOR FILING DATE:  1998-04-09
;  PRIOR APPLICATION NUMBER:  KR 21312/1997
;  PRIOR FILING DATE:  1997-05-28
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 32
;   LENGTH:  22
;   TYPE:  PRT
;   ORGANISM:  Unknown
;   FEATURE:
;   OTHER INFORMATION:  Magainin (MSI-344)
US-09-230-180-32

  Query Match           100.0%;  Score 109;  DB 4;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 3.4e-08;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 GIGKFLKKAKKFGKAFVKILKK 22
              ||||||||||||||||||||||
Db          1 GIGKFLKKAKKFGKAFVKILKK 22


RESULT 5
US-09-115-737-154
; Sequence 154, Application US/09115737
; Patent No. 6348445
;  GENERAL INFORMATION:
;       APPLICANT: U. Prasad Kari
;                  Taffy J. Williams
;                  Michael McLane
;       TITLE OF INVENTION: Biologically Active Peptides With Reduced
;                           Toxicity in Animals and a Method for Preparing Same
;       NUMBER OF SEQUENCES: 156
;       CORRESPONDENCE ADDRESS:
;           ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
;                      Dunner, L.L.P.
;           STREET: 1300 I Street, N.W. Suite 700
;           CITY: Washington
;           STATE: D.C.
;           COUNTRY: USA
;           ZIP: 20005-3315
;       COMPUTER READABLE FORM:
;           MEDIUM TYPE: Floppy disk
;           COMPUTER: IBM PC compatible
;           OPERATING SYSTEM: PC-DOS/MS-DOS
;           SOFTWARE: PatentIn Release #1.0, Version #1.3
;       CURRENT APPLICATION DATA:
;           APPLICATION NUMBER: US/09/115,737
;           FILING DATE: 15-Jul-1998
;           CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;           APPLICATION NUMBER: 08/465,330
;           FILING DATE: 05-JUN-1995
;           APPLICATION NUMBER: 08/184,462
;           FILING DATE: 18-JAN-94
;           APPLICATION NUMBER: 07/891,201
;           FILING DATE: 01-JUN-92
;       ATTORNEY/AGENT INFORMATION:
;           NAME: Fordis, Jean B
;           REGISTRATION NUMBER: 32,984
;           REFERENCE/DOCKET NUMBER: 05387.0021-06000
;       TELECOMMUNICATION INFORMATION:
;           TELEPHONE: (202) 408-4000
;           TELEFAX: (202) 408-4400
;   INFORMATION FOR SEQ ID NO: 154:
;       SEQUENCE CHARACTERISTICS:
;           LENGTH: 22 amino acids
;           TYPE: amino acid
;           STRANDEDNESS: single
;           TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 154:
US-09-115-737-154

  Query Match             100.0%;  Score 109;  DB 4;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-08;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFVKILKK 22
              ||||||||||||||||||||||
Db          1 GIGKFLKKAKKFGKAFVKILKK 22


RESULT 6
PCT-US95-10219-4
; Sequence 4, Application PC/TUS9510219
;  GENERAL INFORMATION:
;    APPLICANT:  Williams, Jon I.
;    APPLICANT:  Pierce, James C.
;    APPLICANT:  Anderson, Mark G.
;    APPLICANT:  Kari, Prasad
;    TITLE OF INVENTION:  Recombinant Production of Biologically
;    TITLE OF INVENTION:  Active Peptides and Proteins
;    NUMBER OF SEQUENCES:  62
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/10219
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/282,030
;      FILING DATE:  29-JUL-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fordis, Jean B.
;      REGISTRATION NUMBER:  32,984
;      REFERENCE/DOCKET NUMBER:  05387.0001-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-408-4000
;      TELEFAX:  202-408-4400
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  22 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
PCT-US95-10219-4

  Query Match             100.0%;  Score 109;  DB 5;  Length 22;
  Best Local Similarity   100.0%;  Pred. No. 3.4e-08;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFVKILKK 22
              ||||||||||||||||||||||
Db          1 GIGKFLKKAKKFGKAFVKILKK 22


RESULT 7
US-07-965-663A-8
; Sequence 8, Application US/07965663A
; Patent No. 5424290
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Maloy W.
;    APPLICANT:  Prasad, Kari U.
;    TITLE OF INVENTION:  No. 5424290el Biologically Active Peptides and
;    TITLE OF INVENTION:  Uses Therefor
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  United States of America
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
```

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;      APPLICATION NUMBER:  US/07/965,663A
;      FILING DATE:  26-OCT-1992
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fordis, Jean B.
;      REGISTRATION NUMBER:  32,984
;      REFERENCE/DOCKET NUMBER:  05387.0039-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-408-4000
;      TELEFAX:  202-408-4400
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      OTHER INFORMATION:  /note= "May be a C-terminal amide, and/or may
US-07-965-663A-8

  Query Match             100.0%;  Score 109;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-08;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFVKILKK 22
              ||||||||||||||||||||||
Db          1 GIGKFLKKAKKFGKAFVKILKK 22


RESULT 8
US-07-965-663A-9
; Sequence 9, Application US/07965663A
; Patent No. 5424290
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Maloy W.
;    APPLICANT:  Prasad, Kari U.
;    TITLE OF INVENTION:  No. 5424290el Biologically Active Peptides and
;    TITLE OF INVENTION:  Uses Therefor
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  United States of America
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/965,663A
;      FILING DATE:  26-OCT-1992
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fordis, Jean B.
;      REGISTRATION NUMBER:  32,984
;      REFERENCE/DOCKET NUMBER:  05387.0039-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-408-4000
;      TELEFAX:  202-408-4400
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      OTHER INFORMATION:  /note= "May be a C-terminal amide, and/or may
US-07-965-663A-9

  Query Match             100.0%;  Score 109;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-08;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFVKILKK 22
              ||||||||||||||||||||||
Db          1 GIGKFLKKAKKFGKAFVKILKK 22


RESULT 9
US-07-965-663A-10
; Sequence 10, Application US/07965663A
; Patent No. 5424290
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Maloy W.
;    APPLICANT:  Prasad, Kari U.
;    TITLE OF INVENTION:  No. 5424290el Biologically Active Peptides and
;    TITLE OF INVENTION:  Uses Therefor
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  United States of America
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/965,663A
;      FILING DATE:  26-OCT-1992
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fordis, Jean B.
;      REGISTRATION NUMBER:  32,984
;      REFERENCE/DOCKET NUMBER:  05387.0039-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-408-4000
;      TELEFAX:  202-408-4400
;  INFORMATION FOR SEQ ID NO:  10:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      NAME/KEY:  Modified-site
;      LOCATION:  23
;      OTHER INFORMATION:  /note= "May be a C-terminal amide,
;      OTHER INFORMATION:  and/or may be acetylated at N-terminus.  Xaa is
;      OTHER INFORMATION:  homoserine."
US-07-965-663A-10

  Query Match             100.0%;  Score 109;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-08;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFVKILKK 22
              ||||||||||||||||||||||
Db          1 GIGKFLKKAKKFGKAFVKILKK 22


RESULT 10
US-07-965-663A-11
; Sequence 11, Application US/07965663A
; Patent No. 5424290
```

```
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Maloy W.
;    APPLICANT:  Prasad, Kari U.
;    TITLE OF INVENTION:  No. 5424290el Biologically Active Peptides and
;    TITLE OF INVENTION:  Uses Therefor
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  United States of America
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/965,663A
;      FILING DATE:  26-OCT-1992
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fordis, Jean B.
;      REGISTRATION NUMBER:  32,984
;      REFERENCE/DOCKET NUMBER:  05387.0039-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-408-4000
;      TELEFAX:  202-408-4400
;  INFORMATION FOR SEQ ID NO:  11:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  23 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      OTHER INFORMATION:  /note= "May be a C-terminal amide, and/or may
US-07-965-663A-11

  Query Match             100.0%;  Score 109;  DB 1;  Length 23;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-08;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFVKILKK 22
              ||||||||||||||||||||||
Db          2 GIGKFLKKAKKFGKAFVKILKK 23


RESULT 11
US-07-965-663A-12
; Sequence 12, Application US/07965663A
; Patent No. 5424290
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Maloy W.
;    APPLICANT:  Prasad, Kari U.
;    TITLE OF INVENTION:  No. 5424290el Biologically Active Peptides and
;    TITLE OF INVENTION:  Uses Therefor
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  United States of America
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/965,663A
;      FILING DATE:  26-OCT-1992
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fordis, Jean B.
;      REGISTRATION NUMBER:  32,984
;      REFERENCE/DOCKET NUMBER:  05387.0039-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-408-4000
;      TELEFAX:  202-408-4400
;  INFORMATION FOR SEQ ID NO:  12:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  24 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      OTHER INFORMATION:  /note= "May be a C-terminal amide, and/or may
US-07-965-663A-12

  Query Match             100.0%;  Score 109;  DB 1;  Length 24;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-08;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFVKILKK 22
              ||||||||||||||||||||||
Db          3 GIGKFLKKAKKFGKAFVKILKK 24


RESULT 12
US-07-965-663A-13
; Sequence 13, Application US/07965663A
; Patent No. 5424290
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Maloy W.
;    APPLICANT:  Prasad, Kari U.
;    TITLE OF INVENTION:  No. 5424290el Biologically Active Peptides and
;    TITLE OF INVENTION:  Uses Therefor
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  United States of America
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/965,663A
;      FILING DATE:  26-OCT-1992
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fordis, Jean B.
;      REGISTRATION NUMBER:  32,984
;      REFERENCE/DOCKET NUMBER:  05387.0039-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-408-4000
;      TELEFAX:  202-408-4400
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  25 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
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```
;      OTHER INFORMATION:  /note= "May be a C-terminal amide, and/or may
US-07-965-663A-13

  Query Match             100.0%;  Score 109;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-08;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFVKILKK 22
              ||||||||||||||||||||||
Db          3 GIGKFLKKAKKFGKAFVKILKK 24


RESULT 13
US-07-965-663A-14
; Sequence 14, Application US/07965663A
; Patent No. 5424290
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Maloy W.
;    APPLICANT:  Prasad, Kari U.
;    TITLE OF INVENTION:  No. 5424290el Biologically Active Peptides and
;    TITLE OF INVENTION:  Uses Therefor
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  United States of America
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/965,663A
;      FILING DATE:  26-OCT-1992
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fordis, Jean B.
;      REGISTRATION NUMBER:  32,984
;      REFERENCE/DOCKET NUMBER:  05387.0039-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-408-4000
;      TELEFAX:  202-408-4400
;  INFORMATION FOR SEQ ID NO:  14:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  25 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      OTHER INFORMATION:  /note= "May be a C-terminal amide, and/or may
US-07-965-663A-14

  Query Match             100.0%;  Score 109;  DB 1;  Length 25;
  Best Local Similarity   100.0%;  Pred. No. 3.8e-08;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFVKILKK 22
              ||||||||||||||||||||||
Db          1 GIGKFLKKAKKFGKAFVKILKK 22


RESULT 14
US-07-965-663A-15
; Sequence 15, Application US/07965663A
; Patent No. 5424290
;  GENERAL INFORMATION:
;    APPLICANT:  Lee, Maloy W.
;    APPLICANT:  Prasad, Kari U.
;    TITLE OF INVENTION:  No. 5424290el Biologically Active Peptides and
;    TITLE OF INVENTION:  Uses Therefor
;    NUMBER OF SEQUENCES:  23
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Finnegan, Henderson, Farabow, Garrett &
;      ADDRESSEE:  Dunner
;      STREET:  1300 I Street, N.W.
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  United States of America
;      ZIP:  20005-3315
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/965,663A
;      FILING DATE:  26-OCT-1992
;      CLASSIFICATION:  514
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Fordis, Jean B.
;      REGISTRATION NUMBER:  32,984
;      REFERENCE/DOCKET NUMBER:  05387.0039-00000
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  202-408-4000
;      TELEFAX:  202-408-4400
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  26 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
;    FEATURE:
;      OTHER INFORMATION:  /note= "May be a C-terminal amide, and/or may
US-07-965-663A-15

  Query Match             100.0%;  Score 109;  DB 1;  Length 26;
  Best Local Similarity   100.0%;  Pred. No. 3.9e-08;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFVKILKK 22
              ||||||||||||||||||||||
Db          1 GIGKFLKKAKKFGKAFVKILKK 22


RESULT 15
US-09-230-180-7
; Sequence 7, Application US/09230180
; Patent No. 6183992
; GENERAL INFORMATION:
;  APPLICANT:  Kim, Sun-Chang
;  APPLICANT:  Lee, Jae Hyun
;  APPLICANT:  Kang, Min Hyung
;  APPLICANT:  Kim, Jeong Hyun
;  APPLICANT:  Hong, Seung-Suh
;  APPLICANT:  Lee, Hyun-Soo
;  APPLICANT:  Samyang Genex Corporation
;  APPLICANT:  Korea Advanced Institute of Science and Technology
;  TITLE OF INVENTION:  METHOD FOR MASS PRODUCTION OF
;  TITLE OF INVENTION:  ANTIMICROBIAL PEPTIDE
;  FILE REFERENCE:  6181/0F135
;  CURRENT APPLICATION NUMBER: US/09/230,180
;  CURRENT FILING DATE:  1999-03-10
;  PRIOR APPLICATION NUMBER:  PCT/KR98/00132
;  PRIOR FILING DATE:  1998-05-28
;  PRIOR APPLICATION NUMBER:  KR 13372/1998
;  PRIOR FILING DATE:  1998-04-09
;  PRIOR APPLICATION NUMBER:  KR 21312/1997
;  PRIOR FILING DATE:  1997-05-28
;  NUMBER OF SEQ ID NOS:  36
;  SOFTWARE:  FastSEQ for Windows Version 3.0
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; SEQ ID NO 7
; LENGTH: 84
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Guamerin/MSI-78 fusion protein
US-09-230-180-7

Query Match 100.0%; Score 109; DB 4; Length 84;
Best Local Similarity 100.0%; Pred. No. 1e-07;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GIGKFLKKAKKFGKAFVKILKK 22
              ||||||||||||||||||||||
Db         63 GIGKFLKKAKKFGKAFVKILKK 84
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Search completed: June 30, 2003, 16:10:13
Job time : 35 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 30, 2003, 16:08:50 ; Search time 50 Seconds
(without alignments)
48.245 Million cell updates/sec

Title: US-09-904-753-4
Perfect score: 109
Sequence: 1 GIGKFLKKAKKFGKAFVKILKK 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 424699 seqs, 109646833 residues

Total number of hits satisfying chosen parameters: 424699

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	109	100.0	22	9	US-09-820-053A-24	Sequence 24, Appl
2	109	100.0	22	9	US-09-904-753-4	Sequence 4, Appli
3	109	100.0	22	9	US-10-109-171-24	Sequence 24, Appl
4	104	95.4	22	9	US-09-904-753-3	Sequence 3, Appli
5	94	86.2	22	9	US-09-807-720-3	Sequence 3, Appli
6	75	68.8	23	9	US-09-820-053A-7	Sequence 7, Appli
7	75	68.8	23	9	US-09-904-753-2	Sequence 2, Appli
8	75	68.8	23	9	US-10-109-171-7	Sequence 7, Appli
9	75	68.8	23	10	US-09-030-619-211	Sequence 211, App
10	75	68.8	303	10	US-09-917-340-4	Sequence 4, Appli
11	69.5	63.8	23	9	US-09-904-753-1	Sequence 1, Appli
12	69.5	63.8	23	10	US-09-030-619-210	Sequence 210, App
13	68	62.4	23	9	US-09-820-053A-146	Sequence 146, App
14	68	62.4	23	9	US-10-109-171-146	Sequence 146, App
15	50	45.9	20	9	US-10-081-418-1	Sequence 1, Appli
16	49	45.0	23	9	US-09-269-882-2	Sequence 2, Appli
17	49	45.0	23	9	US-09-820-053A-147	Sequence 147, App
18	49	45.0	23	9	US-09-820-053A-154	Sequence 154, App
19	49	45.0	23	9	US-10-109-171-147	Sequence 147, App
20	49	45.0	23	9	US-10-109-171-154	Sequence 154, App
21	44.5	40.8	37	9	US-10-060-102-7	Sequence 7, Appli
22	44.5	40.8	39	9	US-10-060-102-6	Sequence 6, Appli
23	44.5	40.8	170	10	US-09-917-340-32	Sequence 32, Appl
24	44	40.4	580	10	US-09-815-242-4959	Sequence 4959, Ap
25	44	40.4	589	10	US-09-815-242-10803	Sequence 10803, A
26	43	39.4	18	9	US-09-865-989-242	Sequence 242, App
27	43	39.4	18	9	US-10-099-574A-242	Sequence 242, App
28	43	39.4	23	9	US-09-820-053A-151	Sequence 151, App
29	43	39.4	23	9	US-10-109-171-151	Sequence 151, App
30	43	39.4	602	10	US-09-841-132-565	Sequence 565, App
31	43	39.4	610	10	US-09-815-242-10414	Sequence 10414, A
32	43	39.4	615	10	US-09-815-242-13747	Sequence 13747, A
33	43	39.4	1249	9	US-09-964-899-33	Sequence 33, Appl
34	43	39.4	1478	10	US-09-801-368-52	Sequence 52, Appl
35	42.5	39.0	1386	10	US-09-866-582-38	Sequence 38, Appl
36	42	38.5	602	10	US-09-841-132-495	Sequence 495, App
37	41.5	38.1	507	10	US-09-729-674-14	Sequence 14, Appl
38	41	37.6	29	9	US-09-908-139-24	Sequence 24, Appl
39	41	37.6	29	10	US-09-917-340-31	Sequence 31, Appl
40	41	37.6	223	10	US-09-815-242-13664	Sequence 13664, A
41	41	37.6	389	9	US-10-151-763-6	Sequence 6, Appli
42	41	37.6	700	9	US-10-153-273-10	Sequence 10, Appl
43	41	37.6	982	9	US-09-991-496-95	Sequence 95, Appl
44	41	37.6	982	10	US-09-874-923-95	Sequence 95, Appl
45	41	37.6	1279	9	US-10-251-385-293	Sequence 293, App

ALIGNMENTS

RESULT 1
US-09-820-053A-24
; Sequence 24, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 22
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (22)
; OTHER INFORMATION: AMIDATION
US-09-820-053A-24

Query Match 100.0%; Score 109; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 1.8e-09;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GIGKFLKKAKKFGKAFVKILKK 22
||||||||||||||||||||||
Db 1 GIGKFLKKAKKFGKAFVKILKK 22

RESULT 2
US-09-904-753-4
; Sequence 4, Application US/09904753
; Publication No. US20030092612A1
; GENERAL INFORMATION:
; APPLICANT: Lynos, Robert T
; TITLE OF INVENTION: Use of ANtimicrobal Peptides as Preservatives in
; TITLE OF INVENTION: Ophthalmic Preparations, Including Solutions,
; TITLE OF INVENTION: Emulsions, and Suspentions
; FILE REFERENCE: 2973 ver 2

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;  CURRENT APPLICATION NUMBER: US/09/904,753
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: WO 96/25183
;  PRIOR FILING DATE: 1996-08-22
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 22
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: maginin analog
US-09-904-753-4

  Query Match           100.0%;  Score 109;  DB 9;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-09;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFVKILKK 22
              ||||||||||||||||||||||
Db          1 GIGKFLKKAKKFGKAFVKILKK 22


RESULT 3
US-10-109-171-24
; Sequence 24, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
;  FILE REFERENCE: HELX028
;  CURRENT APPLICATION NUMBER: US/10/109,171
;  CURRENT FILING DATE:  2002-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;   LENGTH: 22
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC SEQUENCE
;   NAME/KEY: MOD_RES
;   LOCATION: (22)
;   OTHER INFORMATION: AMIDATION
US-10-109-171-24

  Query Match           100.0%;  Score 109;  DB 9;  Length 22;
  Best Local Similarity  100.0%;  Pred. No. 1.8e-09;
  Matches   22;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFVKILKK 22
              ||||||||||||||||||||||
Db          1 GIGKFLKKAKKFGKAFVKILKK 22


RESULT 4
US-09-904-753-3
; Sequence 3, Application US/09904753
; Publication No. US20030092612A1
; GENERAL INFORMATION:
;  APPLICANT: Lynos, Robert T
;  TITLE OF INVENTION: Use of ANtimicrobal Peptides as Preservatives in
;  TITLE OF INVENTION:  Ophthalmic Preparations, Including Solutions,
;  TITLE OF INVENTION:  Emulsions, and Suspentions
;  FILE REFERENCE: 2973 ver 2
;  CURRENT APPLICATION NUMBER: US/09/904,753
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: WO 96/25183
;  PRIOR FILING DATE: 1996-08-22
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 22
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   NAME/KEY: PEPTIDE
;   LOCATION: (22)
;   OTHER INFORMATION: Xaa at position 22 is Lys-amide
;   OTHER INFORMATION: Description of Artificial Sequence: maginin analog
US-09-904-753-3

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  Best Local Similarity  100.0%;  Pred. No. 9.5e-09;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFVKILK 21
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Db          1 GIGKFLKKAKKFGKAFVKILK 21


RESULT 5
US-09-807-720-3
; Sequence 3, Application US/09807720
; Patent No. US20020162135A1
; GENERAL INFORMATION:
;  APPLICANT: DANIELL, HENRY
;  TITLE OF INVENTION: EXPRESSION OF AN ANTIMICROBIAL PEPTIDE VIA THE PLASTID
;  TITLE OF INVENTION:  GENOME TO CONTROL PHYTOPATHOGENIC BACTERIA
;  FILE REFERENCE: 1462-PCT-US-00
;  CURRENT APPLICATION NUMBER: US/09/807,720
;  CURRENT FILING DATE:  2001-04-18
;  PRIOR APPLICATION NUMBER: 60/185,662
;  PRIOR FILING DATE: 2000-02-29
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 22
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: peptide
US-09-807-720-3

  Query Match           86.2%;  Score 94;  DB 9;  Length 22;
  Best Local Similarity  95.0%;  Pred. No. 2.7e-07;
  Matches   19;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFVKIL 20
              ||||||| ||||||||||||
Db          1 GIGKFLKSAKKFGKAFVKIL 20


RESULT 6
US-09-820-053A-7
; Sequence 7, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
;  FILE REFERENCE: HELX027
;  CURRENT APPLICATION NUMBER: US/09/820,053A
;  CURRENT FILING DATE:  2001-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 23
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC SEQUENCE
;   NAME/KEY: MOD_RES
;   LOCATION: (23)
;   OTHER INFORMATION: AMIDATION
US-09-820-053A-7
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  Query Match             68.8%;  Score 75;  DB 9;  Length 23;
  Best Local Similarity   88.2%;  Pred. No. 0.00016;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFV 17
              ||||||  |||||||||
Db          1 GIGKFLHSAKKFGKAFV 17


RESULT 7
US-09-904-753-2
; Sequence 2, Application US/09904753
; Publication No. US20030092612A1
; GENERAL INFORMATION:
;  APPLICANT: Lynos, Robert T
;  TITLE OF INVENTION: Use of ANtimicrobal Peptides as Preservatives in
;  TITLE OF INVENTION:  Ophthalmic Preparations, Including Solutions,
;  TITLE OF INVENTION:  Emulsions, and Suspentions
;  FILE REFERENCE: 2973 ver 2
;  CURRENT APPLICATION NUMBER: US/09/904,753
;  CURRENT FILING DATE:  2001-07-13
;  PRIOR APPLICATION NUMBER: WO 96/25183
;  PRIOR FILING DATE: 1996-08-22
;  NUMBER OF SEQ ID NOS: 14
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 23
;   TYPE: PRT
;   ORGANISM: Xenopus laevis
US-09-904-753-2

  Query Match             68.8%;  Score 75;  DB 9;  Length 23;
  Best Local Similarity   88.2%;  Pred. No. 0.00016;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFV 17
              ||||||  |||||||||
Db          1 GIGKFLHSAKKFGKAFV 17


RESULT 8
US-10-109-171-7
; Sequence 7, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
;  APPLICANT: Owen, Donald R.
;  TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
;  FILE REFERENCE: HELX028
;  CURRENT APPLICATION NUMBER: US/10/109,171
;  CURRENT FILING DATE:  2002-03-28
;  NUMBER OF SEQ ID NOS: 165
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
;   LENGTH: 23
;   TYPE: PRT
;   ORGANISM: ARTIFICIAL SEQUENCE
;   FEATURE:
;   OTHER INFORMATION: SYNTHETIC SEQUENCE
;   NAME/KEY: MOD_RES
;   LOCATION: (23)
;   OTHER INFORMATION: AMIDATION
US-10-109-171-7

  Query Match             68.8%;  Score 75;  DB 9;  Length 23;
  Best Local Similarity   88.2%;  Pred. No. 0.00016;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFV 17
              ||||||  |||||||||
Db          1 GIGKFLHSAKKFGKAFV 17


RESULT 9
US-09-030-619-211
; Sequence 211, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
;  APPLICANT:  Krieger, Timothy J.
;  APPLICANT:  Taylor, Robert
;  APPLICANT:  Erfle, Douglas
;  APPLICANT:  Fraser, Janet R.
;  APPLICANT:  West, Michael H.P.
;  APPLICANT:  McNicol, Patricia J.
;  TITLE OF INVENTION:  COMPOSITIONS AND METHODS FOR TREATING
;  TITLE OF INVENTION:  INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
;  TITLE OF INVENTION:  WITH ANTIBIOTICS
;  FILE REFERENCE:  660081.406
;  CURRENT APPLICATION NUMBER: US/09/030,619B
;  CURRENT FILING DATE:  1998-02-25
;  NUMBER OF SEQ ID NOS:  232
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 211
;   LENGTH: 23
;   TYPE: PRT
;   ORGANISM: Xenopus laevis
US-09-030-619-211

  Query Match             68.8%;  Score 75;  DB 10;  Length 23;
  Best Local Similarity   88.2%;  Pred. No. 0.00016;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFV 17
              ||||||  |||||||||
Db          1 GIGKFLHSAKKFGKAFV 17


RESULT 10
US-09-917-340-4
; Sequence 4, Application US/09917340
; Patent No. US20020090369A1
; GENERAL INFORMATION:
;  APPLICANT: Murphy, Christopher J.
;  APPLICANT:  McAnulty, Jonathan F.
;  APPLICANT:  Reid, Ted W.
;  TITLE OF INVENTION: Transplant Media
;  FILE REFERENCE: TPLANT-06468
;  CURRENT APPLICATION NUMBER: US/09/917,340
;  CURRENT FILING DATE:  2001-07-29
;  PRIOR APPLICATION NUMBER: 60/221,632
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: 60/249,602
;  PRIOR FILING DATE: 2000-11-17
;  PRIOR APPLICATION NUMBER: 60/290,932
;  PRIOR FILING DATE: 2001-05-15
;  NUMBER OF SEQ ID NOS: 96
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
;   LENGTH: 303
;   TYPE: PRT
;   ORGANISM: Xenopus laevis
US-09-917-340-4

  Query Match             68.8%;  Score 75;  DB 10;  Length 303;
  Best Local Similarity   88.2%;  Pred. No. 0.0021;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFV 17
              ||||||  |||||||||
Db         83 GIGKFLHSAKKFGKAFV 99


RESULT 11
US-09-904-753-1
; Sequence 1, Application US/09904753
; Publication No. US20030092612A1
```

; GENERAL INFORMATION:
; APPLICANT: Lynos, Robert T
; TITLE OF INVENTION: Use of ANtimicrobal Peptides as Preservatives in
; TITLE OF INVENTION: Ophthalmic Preparations, Including Solutions,
; TITLE OF INVENTION: Emulsions, and Suspentions
; FILE REFERENCE: 2973 ver 2
; CURRENT APPLICATION NUMBER: US/09/904,753
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: WO 96/25183
; PRIOR FILING DATE: 1996-08-22
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Xenopus laevis
; PUBLICATION INFORMATION:
; AUTHORS: Lee et al.,
; TITLE: High-Level Expression of Antimicrobal Peptide Mediated
; TITLE: by a Fusion Partner Reinforcing Formation of Inclusion
; TITLE: Bodies
; JOURNAL: Biochem. Biophys. Res. Commun.
; VOLUME: 277
; PAGES: 575-580
; DATE: Sept 21, 2000
US-09-904-753-1

Query Match 63.8%; Score 69.5; DB 9; Length 23;
Best Local Similarity 72.7%; Pred. No. 0.00099;
Matches 16; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 1 GIGKFLKKAKKFGKAFV-KILK 21
|||||| | ||||||| :|:|
Db 1 GIGKFLHSAGKFGKAFVGEIMK 22

RESULT 12
US-09-030-619-210
; Sequence 210, Application US/09030619B
; Patent No. US20020035061A1
; GENERAL INFORMATION:
; APPLICANT: Krieger, Timothy J.
; APPLICANT: Taylor, Robert
; APPLICANT: Erfle, Douglas
; APPLICANT: Fraser, Janet R.
; APPLICANT: West, Michael H.P.
; APPLICANT: McNicol, Patricia J.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: INFECTIONS USING CATIONIC PEPTIDES ALONE OR IN COMBINATION
; TITLE OF INVENTION: WITH ANTIBIOTICS
; FILE REFERENCE: 660081.406
; CURRENT APPLICATION NUMBER: US/09/030,619B
; CURRENT FILING DATE: 1998-02-25
; NUMBER OF SEQ ID NOS: 232
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 210
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-09-030-619-210

Query Match 63.8%; Score 69.5; DB 10; Length 23;
Best Local Similarity 72.7%; Pred. No. 0.00099;
Matches 16; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

Qy 1 GIGKFLKKAKKFGKAFV-KILK 21
|||||| | ||||||| :|:|
Db 1 GIGKFLHSAGKFGKAFVGEIMK 22

RESULT 13
US-09-820-053A-146
; Sequence 146, Application US/09820053A
; Publication No. US20030083243A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES
; FILE REFERENCE: HELX027
; CURRENT APPLICATION NUMBER: US/09/820,053A
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 146
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (23)
; OTHER INFORMATION: AMIDATION
US-09-820-053A-146

Query Match 62.4%; Score 68; DB 9; Length 23;
Best Local Similarity 82.4%; Pred. No. 0.0016;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GIGKFLKKAKKFGKAFV 17
|||||| |||| ||||
Db 1 GIGKFLHAAKKFAKAFV 17

RESULT 14
US-10-109-171-146
; Sequence 146, Application US/10109171
; Publication No. US20030109452A1
; GENERAL INFORMATION:
; APPLICANT: Owen, Donald R.
; TITLE OF INVENTION: SHORT BIOACTIVE PEPTIDES AND METHODS FOR THEIR USE
; FILE REFERENCE: HELX028
; CURRENT APPLICATION NUMBER: US/10/109,171
; CURRENT FILING DATE: 2002-03-28
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 146
; LENGTH: 23
; TYPE: PRT
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: SYNTHETIC SEQUENCE
; NAME/KEY: MOD_RES
; LOCATION: (23)
; OTHER INFORMATION: AMIDATION
US-10-109-171-146

Query Match 62.4%; Score 68; DB 9; Length 23;
Best Local Similarity 82.4%; Pred. No. 0.0016;
Matches 14; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 GIGKFLKKAKKFGKAFV 17
|||||| |||| ||||
Db 1 GIGKFLHAAKKFAKAFV 17

RESULT 15
US-10-081-418-1
; Sequence 1, Application US/10081418
; Publication No. US20030096745A1
; GENERAL INFORMATION:
; APPLICANT: HAHM, Kyung-Soo
; APPLICANT: LEE, Dong Gun
; APPLICANT: PARK, YoonKyung
; APPLICANT: KIM, Hee Nam
; TITLE OF INVENTION: No. US20030096745A1el peptides with increased + charge and hyd
; TITLE OF INVENTION: substituting one or more amino acids of CA-MA peptide and
; TITLE OF INVENTION: pharmaceutical compositions containing thereof

; FILE REFERENCE: 428.1014
; CURRENT APPLICATION NUMBER: US/10/081,418
; CURRENT FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: KopatentIn 1.71
; SEQ ID NO 1
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CA-MA peptide made by fusing 1-8 amino acid of secropin A and
; OTHER INFORMATION: 1-12 amino acid of magainin 2
US-10-081-418-1

Query Match 45.9%; Score 50; DB 9; Length 20;
Best Local Similarity 83.3%; Pred. No. 0.58;
Matches 10; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 GIGKFLKKAKKF 12
              ||||||  ||||
Db          9 GIGKFLHSAKKF 20
```

Search completed: June 30, 2003, 16:15:25
Job time : 51 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 30, 2003, 16:06:00 ; Search time 39 Seconds
(without alignments)
54.230 Million cell updates/sec

Title: US-09-904-753-4
Perfect score: 109
Sequence: 1 GIGKFLKKAKKFGKAFVKILKK 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	75	68.8	303	2	A28620	magainin precursor
2	53	48.6	787	2	C75068	probable beta-gala
3	48	44.0	129	2	B82368	hypothetical prote
4	47	43.1	226	2	E90246	conserved hypothet
5	47	43.1	527	1	S18762	outer capsid prote
6	46	42.2	227	2	E64306	hypothetical prote
7	46	42.2	276	2	D90595	hypothetical prote
8	46	42.2	409	2	T17258	hypothetical prote
9	46	42.2	462	2	AB1069	chain S of type I
10	45	41.3	179	2	AF0030	probable DNA-bindi
11	45	41.3	201	2	A31484	troponin I, fast s
12	45	41.3	208	2	A38594	troponin I - fruit
13	45	41.3	208	2	A40547	troponin I - fruit
14	45	41.3	260	2	B38594	troponin I - fruit
15	45	41.3	627	2	E69504	conserved hypothet
16	45	41.3	897	2	C90561	hypothetical prote
17	45	41.3	982	2	I64232	protein p115 homol
18	45	41.3	1039	2	E72734	hypothetical prote
19	45	41.3	1437	2	F69680	DNA-directed DNA p
20	45	41.3	2269	2	T28677	rhoptry protein -
21	44.5	40.8	170	2	S74248	antibacterial pept
22	44.5	40.8	170	2	I38932	CAP18 precursor -
23	44.5	40.8	379	2	B69393	glutamate N-acetyl
24	44	40.4	156	2	AF1784	conserved hypothet
25	44	40.4	156	2	AH1408	conserved hypothet
26	44	40.4	343	1	C70418	probable alcohol d
27	44	40.4	391	2	E44490	retrovirus-related
28	44	40.4	479	1	JN0715	3-phytase (EC 3.1.
29	44	40.4	479	1	JN0890	acid phosphatase (
30	44	40.4	538	2	A54391	translation initia
31	43	39.4	75	2	D97813	hypothetical prote
32	43	39.4	191	2	S70271	outer surface prot
33	43	39.4	194	2	S64075	probable ribosomal
34	43	39.4	209	2	I40270	outer surface prot
35	43	39.4	217	2	B70330	hypothetical prote
36	43	39.4	249	2	D81377	tryptophan synthas
37	43	39.4	253	2	H81690	conserved hypothet
38	43	39.4	315	2	E96971	cobyrinic acid a,c
39	43	39.4	332	2	A86892	glycosyltransferas
40	43	39.4	438	2	S73608	arginine deiminase
41	43	39.4	602	2	B71561	probable GTPase -
42	43	39.4	602	2	B81714	GTP-binding protei
43	43	39.4	606	2	T47690	hypothetical prote
44	43	39.4	609	2	AH0917	ATP-dependent DNA
45	43	39.4	610	1	BVECRQ	DNA helicase recQ

ALIGNMENTS

RESULT 1
A28620
magainin precursor - African clawed frog
N;Contains: magainin 1; magainin 2
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 18-Aug-2000
C;Accession: A28620; A29771
R;Terry, A.S.; Poulter, L.; Williams, D.H.; Nutkins, J.C.; Giovannini, M.G.; Moore, C
J. Biol. Chem. 263, 5745-5751, 1988
A;Title: The cDNA sequence coding for prepro-PGS (prepro-magainins) and aspects of th
A;Reference number: A28620; MUID:88186892; PMID:2833514
A;Accession: A28620
A;Molecule type: mRNA
A;Residues: 1-303 <TER>
A;Cross-references: GB:J03193; NID:g214654; PIDN:AAA49930.1; PID:g214655
R;Zasloff, M.
Proc. Natl. Acad. Sci. U.S.A. 84, 5449-5453, 1987
A;Title: Magainins, a class of antimicrobial peptides from Xenopus skin: isolation, c
A;Reference number: A29771; MUID:87261003; PMID:3299384
A;Accession: A29771
A;Molecule type: mRNA
A;Residues: 6-73,'Q',75-158,297-303 <ZAS>
C;Superfamily: magainin precursor

Query Match 68.8%; Score 75; DB 2; Length 303;
Best Local Similarity 88.2%; Pred. No. 0.0037;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 GIGKFLKKAKKFGKAFV 17
              |||||| |||||||||
Db         83 GIGKFLHSAKKFGKAFV 99
```

RESULT 2
C75068
probable beta-galactosidase (EC 3.2.1.23) PAB1349 [similarity] - Pyrococcus abyssi (s
N;Alternate names: lactase
C;Species: Pyrococcus abyssi
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 31-Mar-2000
C;Accession: C75068
R;anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s
A;Reference number: A75001
A;Accession: C75068
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-787 <KAW>
A;Cross-references: GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB50440.1; PID:e151
A;Experimental source: strain Orsay
C;Genetics:
A;Gene: PAB1349

```
C;Keywords: glycosidase; hydrolase

  Query Match             48.6%;  Score 53;  DB 2;  Length 787;
  Best Local Similarity   64.7%;  Pred. No. 11;
  Matches   11;  Conservative    2;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IGKFLKKAKKFGKAFVK 18
              |||||:  | |||: ||
Db        422 IGKFLRSNKDFGKSEVK 438


RESULT 3
B82368
hypothetical protein VC0074 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: B82368
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: B82368
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 <HEI>
A;Cross-references: GB:AE004098; GB:AE003852; NID:g9654462; PIDN:AAF93252.1; GSPDB:GN001
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC0074
A;Map position: 1

  Query Match             44.0%;  Score 48;  DB 2;  Length 129;
  Best Local Similarity   58.8%;  Pred. No. 11;
  Matches   10;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          6 LKKAKKFGKAFVKILKK 22
              ||| :|| |   |:|||
Db         80 LKKQRKFHKKLEKVLKK 96


RESULT 4
E90246
conserved hypothetical protein [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001
C;Accession: E90246
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: E90246
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-226 <KUR>
A;Cross-references: GB:AE006641; NID:g13814134; PIDN:AAK41228.1; GSPDB:GN00155
C;Genetics:
A;Gene: SSO0954

  Query Match             43.1%;  Score 47;  DB 2;  Length 226;
  Best Local Similarity   38.9%;  Pred. No. 24;
  Matches    7;  Conservative    7;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 KFLKKAKKFGKAFVKILK 21
              :|||:| |:|: :| : :
Db         99 EFLKEASKYGRVYVTVAR 116


RESULT 5
S18762
outer capsid protein VP5 - epizootic hemorrhagic disease virus (serotype 1, strain US
C;Species: epizootic hemorrhagic disease virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C;Accession: S18762; S26752
R;Iwata, H.; Hirasawa, T.; Roy, P.
Virus Res. 20, 273-281, 1991
A;Title: Complete nucleotide sequence of segment 5 of epizootic haemorrhagic disease
A;Reference number: S18762; MUID:92116632; PMID:1662845
A;Accession: S18762
A;Molecule type: genomic RNA
A;Residues: 1-527 <IWA>
A;Cross-references: EMBL:X55782
R;Roy, P.
submitted to the EMBL Data Library, November 1990
A;Reference number: S26752
A;Accession: S26752
A;Molecule type: genomic RNA
A;Residues: 1-392,'S',394-527 <ROY>
A;Cross-references: EMBL:X55782; NID:g59227; PIDN:CAA39303.1; PID:g59228
C;Genetics:
A;Map position: segment 5
C;Superfamily: bluetongue virus outer capsid protein VP5
C;Keywords: capsid protein; coat protein; glycoprotein
F;390,484/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             43.1%;  Score 47;  DB 1;  Length 527;
  Best Local Similarity   61.5%;  Pred. No. 53;
  Matches    8;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 IGKFLKKAKKFGK 14
              :|||:|:  ||||
Db          1 MGKFIKQLSKFGK 13


RESULT 6
E64306
hypothetical protein MJ0053 - Methanococcus jannaschii
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 22-Oct-1999
C;Accession: E64306
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek,
rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc
A;Reference number: A64300; MUID:96337999; PMID:8688087
A;Accession: E64306
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-227 <BUL>
A;Cross-references: GB:U67463; GB:L77117; NID:g1590846; PIDN:AAB98039.1; PID:g1498814
C;Genetics:
A;Map position: REV54068-53385

  Query Match             42.2%;  Score 46;  DB 2;  Length 227;
  Best Local Similarity   58.8%;  Pred. No. 34;
  Matches   10;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IGKFLKKAKKFGKAFVK 18
              | |.::|||||| | |:
Db         68 INKEIEKAKKFGYAVVE 84


RESULT 7
D90595
hypothetical protein MYPU_6680 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C;Species: Mycoplasma pulmonis
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C;Accession: D90595
R;Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer,
Nucleic Acids Res. 29, 2145-2153, 2001
A;Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma p
```

```
A;Reference number: A99512; MUID:21267165; PMID:11353084
A;Accession: D90595
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-276 <KUR>
A;Cross-references: GB:AL445566; PID:g14090083; PIDN:CAC13841.1; GSPDB:GN00153
A;Experimental source: strain UAB CTIP
C;Genetics:
A;Gene: MYPU_6680
A;Genetic code: SGC3

  Query Match             42.2%;  Score 46;  DB 2;  Length 276;
  Best Local Similarity   69.2%;  Pred. No. 41;
  Matches    9;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 KFLKKAKKFGKAF 16
              ||: ||| | |||
Db         26 KFIVKAKSFSKAF 38


RESULT 8
T17258
hypothetical protein DKFZp727A071.1 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Nov-2000
C;Accession: T17258
R;Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, September 1999
A;Reference number: Z18723
A;Accession: T17258
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-409 <POU>
A;Cross-references: EMBL:AL117473
A;Experimental source: adult breast cancer; clone DKFZp727A071
C;Genetics:
A;Note: DKFZp727A071.1
C;Superfamily: proline-tRNA ligase proS

  Query Match             42.2%;  Score 46;  DB 2;  Length 409;
  Best Local Similarity   57.1%;  Pred. No. 58;
  Matches   12;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          2 IGKFLKKAKKFGKAFVKILKK 22
              ||  || | |||  || |  |
Db        352 IGNRLKDANKFGYPFVIIAGK 372


RESULT 9
AB1069
chain S of type I restriction-modification system [imported] - Salmonella enterica subsp
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C;Accession: AB1069
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Accession: AB1069
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-462 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD03369.1; PID:g16505640; GSPDB:GN00176
C;Genetics:
A;Gene: hsdS
C;Superfamily: type I site-specific deoxyribonuclease EcoK chain S

  Query Match             42.2%;  Score 46;  DB 2;  Length 462;
  Best Local Similarity   64.3%;  Pred. No. 65;
  Matches    9;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IGKFLKKAKKFGKA 15
              :|| | ||| || |
Db        239 LGKMLDKAKNFGSA 252


RESULT 10
AF0030
probable DNA-binding protein YPO0245 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C;Accession: AF0030
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrel
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AF0030
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-179 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC89105.1; PID:g15978345; GSPDB:GN00175
C;Genetics:
A;Gene: YPO0245

  Query Match             41.3%;  Score 45;  DB 2;  Length 179;
  Best Local Similarity   50.0%;  Pred. No. 38;
  Matches    8;  Conservative    3;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAF 16
              | || |::  :||| |
Db        108 GQGKLLQRKSRFGKVF 123


RESULT 11
A31484
troponin I, fast skeletal muscle - broad-fingered crayfish
C;Species: Astacus astacus, Astacus fluviatilis (broad-fingered crayfish)
C;Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 07-Feb-1997
C;Accession: A31484
R;Kobayashi, T.; Takagi, T.; Konishi, K.; Cox, J.A.
J. Biol. Chem. 264, 1551-1557, 1989
A;Title: Amino acid sequence of crayfish troponin I.
A;Reference number: A31484; MUID:89109165; PMID:2912973
A;Accession: A31484
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-201 <KOB>
C;Superfamily: troponin I
C;Keywords: actin binding; skeletal muscle

  Query Match             41.3%;  Score 45;  DB 2;  Length 201;
  Best Local Similarity   45.8%;  Pred. No. 42;
  Matches   11;  Conservative    2;  Mismatches    7;  Indels    4;  Gaps    1;

Qy          3 GKF----LKKAKKFGKAFVKILKK 22
              |||    |||  |:   | |: ||
Db        138 GKFIKPTLKKVSKYENKFAKLQKK 161


RESULT 12
A38594
troponin I - fruit fly (Drosophila melanogaster) (clone E2)
C;Species: Drosophila melanogaster
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 13-Aug-1999
C;Accession: A38594
R;Barbas, J.A.; Galceran, J.; Krah-Jentgens, I.; de la Pompa, J.L.; Canal, I.; Pongs,
Genes Dev. 5, 132-140, 1991
A;Title: Troponin I is encoded in the haplolethal region of the Shaker gene complex o
A;Reference number: A38594; MUID:91115093; PMID:1899228
A;Accession: A38594
```

A;Molecule type: DNA
A;Residues: 1-208 <BAR>
A;Cross-references: GB:X58188; NID:g2511643; PIDN:CAA41171.1; PID:g8738
C;Genetics:
A;Gene: FlyBase:wupA
A;Cross-references: FlyBase:FBgn0004028
A;Introns: 5/3; 123/3; 185/3
C;Superfamily: troponin I

Query Match 41.3%; Score 45; DB 2; Length 208;
Best Local Similarity 45.8%; Pred. No. 43;
Matches 11; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

Qy 3 GKF----LKKAKKFGKAFVKILKK 22
||| ||| |: | |: ||
Db 136 GKFVKPALKKVSKYENKFAKLQKK 159

RESULT 13
A40547
troponin I - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 28-May-1992 #sequence_revision 28-May-1992 #text_change 13-Aug-1999
C;Accession: A40547
R;Beall, C.J.; Fyrberg, E.
J. Cell Biol. 114, 941-951, 1991
A;Title: Muscle abnormalities in Drosophila melanogaster heldup mutants are caused by mi
A;Reference number: A40547; MUID:91340840; PMID:1908472
A;Accession: A40547
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: mRNA
A;Residues: 1-208 <BEA>
A;Cross-references: GB:X59376; NID:g8057; PIDN:CAA42020.1; PID:g8058
C;Genetics:
A;Gene: FlyBase:wupA
A;Cross-references: FlyBase:FBgn0004028
C;Superfamily: troponin I

Query Match 41.3%; Score 45; DB 2; Length 208;
Best Local Similarity 45.8%; Pred. No. 43;
Matches 11; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

Qy 3 GKF----LKKAKKFGKAFVKILKK 22
||| ||| |: | |: ||
Db 136 GKFVKPALKKVSKYENKFAKLQKK 159

RESULT 14
B38594
troponin I - fruit fly (Drosophila melanogaster) (clone A16)
C;Species: Drosophila melanogaster
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Feb-1997
C;Accession: B38594
R;Barbas, J.A.; Galceran, J.; Krah-Jentgens, I.; de la Pompa, J.L.; Canal, I.; Pongs, O.
Genes Dev. 5, 132-140, 1991
A;Title: Troponin I is encoded in the haplolethal region of the Shaker gene complex of D
A;Reference number: A38594; MUID:91115093; PMID:1899228
A;Accession: B38594
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-260 <BAR>
A;Cross-references: GB:X58188
C;Genetics:
A;Gene: FlyBase:wupA
A;Cross-references: FlyBase:FBgn0004028
C;Superfamily: troponin I

Query Match 41.3%; Score 45; DB 2; Length 260;
Best Local Similarity 45.8%; Pred. No. 53;
Matches 11; Conservative 2; Mismatches 7; Indels 4; Gaps 1;

Qy 3 GKF---LKKAKKFGKAFVKILKK 22
||| ||| |: | |: ||
Db 197 GKFVKPALKKVSKYENKFAKLQKK 220

RESULT 15
E69504
conserved hypothetical protein AF2038 - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 29-Sep-1999
C;Accession: E69504
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes,
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: E69504
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-627 <KLE>
A;Cross-references: GB:AE000962; GB:AE000782; NID:g2689285; PIDN:AAB89216.1; PID:g264
C;Superfamily: hypothetical protein YPL009c

Query Match 41.3%; Score 45; DB 2; Length 627;
Best Local Similarity 47.4%; Pred. No. 1.2e+02;
Matches 9; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 4 KFLKKAKKFGKAFVKILKK 22
|| |:| :| || :|:|
Db 59 KFPKQAPRFPSAFAMLLRK 77

Search completed: June 30, 2003, 16:09:31
Job time : 41 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 30, 2003, 15:59:54 ; Search time 23 Seconds
(without alignments)
39.673 Million cell updates/sec

Title: US-09-904-753-4
Perfect score: 109
Sequence: 1 GIGKFLKKAKKFGKAFVKILKK 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	75	68.8	303	1	MAGA_XENLA	P11006 xenopus lae
2	48.5	44.5	272	1	TYPH_MYCHO	P43050 mycoplasma
3	47	43.1	527	1	VP5_EHDV1	Q01175 epizootic h
4	46	42.2	227	1	Y053_METJA	Q60360 methanococc
5	45	41.3	201	1	TRI_PONLE	P05547 pontastacus
6	45	41.3	268	1	TRI_DROME	P36188 drosophila
7	45	41.3	982	1	P115_MYCGE	P47540 mycoplasma
8	45	41.3	1437	1	DPO3_BACSU	P13267 bacillus su
9	44.5	40.8	170	1	FA39_HUMAN	P49913 homo sapien
10	44	40.4	392	1	PO14_NASVI	Q03272 nasonia vit
11	44	40.4	479	1	PHYB_ASPAW	P34755 aspergillus
12	44	40.4	479	1	PHYB_ASPNG	P34754 aspergillus
13	44	40.4	538	1	IF3C_EUGGR	P36177 euglena gra
14	43	39.4	194	1	YGG8_YEAST	P53163 saccharomyc
15	43	39.4	438	1	ARCX_MYCPN	P75218 mycoplasma
16	43	39.4	602	1	LEPA_CHLMU	Q9pkx6 chlamydia m
17	43	39.4	602	1	LEPA_CHLTR	O84067 chlamydia t
18	43	39.4	607	1	RECQ_ECOLI	P15043 escherichia
19	43	39.4	608	1	RECQ_SALTY	P40724 salmonella
20	43	39.4	1478	1	BCK1_YEAST	Q01389 saccharomyc
21	42	38.5	130	1	RK12_CYACA	Q9tlz9 cyanidium c
22	42	38.5	158	1	MB27_BOVIN	P54228 bos taurus
23	42	38.5	262	1	TRPC_CLOAB	Q97ef3 clostridium
24	42	38.5	330	1	PORB_PYRFU	Q51805 pyrococcus
25	42	38.5	401	1	P39_BRUAB	O06875 brucella ab
26	42	38.5	602	1	LEPA_CHLPN	Q9z8i4 chlamydia p
27	42	38.5	1066	1	SYI_PYRHO	O58792 pyrococcus
28	42	38.5	1067	1	SYI_PYRAB	Q9v072 pyrococcus
29	41.5	38.1	227	1	YG24_HAEIN	P44276 haemophilus
30	41.5	38.1	293	1	KHSE_HELPJ	Q9zm48 helicobacte
31	41.5	38.1	293	1	KHSE_HELPY	O25690 helicobacte
32	41	37.6	29	1	CERB_CERCA	P36191 ceratitis c
33	41	37.6	98	1	C552_HYDTH	P15452 hydrogenoba
34	41	37.6	311	1	DO34_YEAST	P33309 saccharomyc
35	41	37.6	385	1	Y464_MYCGE	P47702 mycoplasma
36	41	37.6	550	1	MANB_MYCGE	P47299 mycoplasma
37	41	37.6	882	1	YBAH_SCHPO	O42908 schizosacch
38	41	37.6	1039	1	SYI_METJA	Q58357 methanococc
39	40.5	37.2	125	1	ACPS_NEIMA	Q9rqw2 neisseria m
40	40.5	37.2	138	1	RL27_SOLTU	P41101 solanum tub
41	40.5	37.2	247	1	STC1_HUMAN	P52823 homo sapien
42	40.5	37.2	247	1	STC1_MOUSE	O55183 mus musculu
43	40.5	37.2	247	1	STC1_RAT	P97574 rattus norv
44	40.5	37.2	507	1	ALG6_HUMAN	Q9y672 homo sapien
45	40.5	37.2	4128	1	PRKD_MOUSE	P97313 mus musculu

ALIGNMENTS

RESULT 1
MAGA_XENLA
ID MAGA_XENLA STANDARD; PRT; 303 AA.
AC P11006;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Magainins precursor.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=88186892; PubMed=2833514;
RA Terry A.S., Poulter L., Williams D.H., Nutkins J.C., Giovannini M.G.,
RA Moore C.H., Gibson B.W.;
RT "The cDNA sequence coding for prepro-PGS (prepro-magainins) and
RT aspects of the processing of this prepro-polypeptide.";
RL J. Biol. Chem. 263:5745-5751(1988).
RN [2]
RP SEQUENCE OF 6-158 AND 297-303 FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=87261003; PubMed=3299384;
RA Zasloff M.;
RT "Magainins, a class of antimicrobial peptides from Xenopus skin:
RT isolation, characterization of two active forms, and partial cDNA
RT sequence of a precursor.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:5449-5453(1987).
RN [3]
RP SEQUENCE OF MAGAININS I AND II.
RC TISSUE=Stomach;
RX MEDLINE=92011794; PubMed=1717472;
RA Moore K.S., Bevins C.L., Brasseur M.M., Tomassini N., Turner K.,
RA Eck H., Zasloff M.;
RT "Antimicrobial peptides in the stomach of Xenopus laevis.";
RL J. Biol. Chem. 266:19851-19857(1991).
RN [4]
RP STRUCTURE BY NMR OF MAGAININ II.
RX MEDLINE=94129391; PubMed=8298457;
RA Bechinger B., Zasloff M., Opella S.J.;
RT "Structure and orientation of the antibiotic peptide magainin in
RT membranes by solid-state nuclear magnetic resonance spectroscopy.";
RL Protein Sci. 2:2077-2084(1993).
CC -!- FUNCTION: ANTIMICROBIAL PEPTIDES THAT INHIBIT THE GROWTH OF
CC NUMEROUS SPECIES OF BACTERIA AND FUNGI AND INDUCE OSMOTIC LYSIS
CC OF PROTOZOA. MAGAININS ARE MEMBRANE LYTIC AGENTS.
CC -!- TISSUE SPECIFICITY: SYNTHESIZED IN THE STOMACH AND STORED IN A
CC NOVEL GRANULAR MULTINUCLEATED CELL IN THE GASTRIC MUCOSA. IT IS
CC STORED AS ACTIVE, PROCESSED PEPTIDES IN LARGE GRANULES WITHIN
CC THE GRANULAR GLAND SECRETIONS OF THE SKIN.
CC -!- SIMILARITY: BELONGS TO THE MAGAININ FAMILY OF ANTIMICROBIAL
CC PEPTIDES.
CC -!- DATABASE: NAME=Protein Spotlight;
CC NOTE=Issue 7 of February 2001;
CC WWW="http://www.expasy.org/spotlight/articles/sptlt007.html".

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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; J03193; AAA49930.1; -.
DR   PIR; A28620; A28620.
DR   PIR; A29771; A29771.
DR   PDB; 2MAG; 08-APR-98.
DR   InterPro; IPR001651; Gastrin.
DR   Pfam; PF00918; Gastrin; 1.
KW   Cleavage on pair of basic residues; Repeat; Amphibian skin;
KW   Antibiotic; Fungicide; Hemolysis; Signal; 3D-structure.
FT   SIGNAL       1     18       POTENTIAL.
FT   PROPEP      19     26
FT   PEPTIDE     27     32       SMALL ACIDIC PEPTIDE COPY A.
FT   PROPEP      33     36
FT   PEPTIDE     37     59       MAGAININ I.
FT   PROPEP      62     72
FT   PEPTIDE     73     78       SMALL ACIDIC PEPTIDE COPY B.
FT   PROPEP      79     82
FT   PEPTIDE     83    105       MAGAININ II COPY A.
FT   PROPEP     108    118
FT   PEPTIDE    119    124       SMALL ACIDIC PEPTIDE COPY C.
FT   PROPEP     125    128
FT   PEPTIDE    129    151       MAGAININ II COPY B.
FT   PROPEP     154    164
FT   PEPTIDE    165    170       SMALL ACIDIC PEPTIDE COPY D.
FT   PROPEP     171    174
FT   PEPTIDE    175    197       MAGAININ II COPY C.
FT   PROPEP     200    210
FT   PEPTIDE    211    216       SMALL ACIDIC PEPTIDE COPY E.
FT   PROPEP     217    220
FT   PEPTIDE    221    243       MAGAININ II COPY D.
FT   PROPEP     246    256
FT   PEPTIDE    257    262       SMALL ACIDIC PEPTIDE COPY F.
FT   PROPEP     263    266
FT   PEPTIDE    267    289       MAGAININ II COPY E.
FT   PROPEP     292    303
FT   CONFLICT    74     74       E -> Q (IN REF. 2).
SQ   SEQUENCE   303 AA;  33379 MW;  E369B0DBB033EA80 CRC64;

  Query Match             68.8%;  Score 75;  DB 1;  Length 303;
  Best Local Similarity   88.2%;  Pred. No. 0.00054;
  Matches   15;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFV 17
              ||||||  |||||||||
Db         83 GIGKFLHSAKKFGKAFV 99


RESULT 2
TYPH_MYCHO
ID   TYPH_MYCHO     STANDARD;      PRT;   272 AA.
AC   P43050;
DT   01-NOV-1995 (Rel. 32, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   Thymidine phosphorylase (EC 2.4.2.4) (TDRPASE) (Fragment).
GN   DEOA.
OS   Mycoplasma hominis.
OC   Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX   NCBI_TaxID=2098;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=FBG;
RA   Schuchart K.;
RL   Thesis (1993), Heinrich-Heine University / Duesseldorf, Germany.
CC   -!- FUNCTION: THE ENZYMES WHICH CATALYZE THE REVERSIBLE PHOSPHORYLOSIS
CC       OF PYRIMIDINE NUCLEOSIDES ARE INVOLVED IN THE DEGRADATION OF THESE
CC       COMPOUNDS AND IN THEIR UTILIZATION AS CARBON AND ENERGY SOURCES,
CC       OR IN THE RESCUE OF PYRIMIDINE BASES FOR NUCLEOTIDE SYNTHESIS.
CC   -!- CATALYTIC ACTIVITY: Thymidine + phosphate = thymine + 2-deoxy-D-
CC       ribose 1-phosphate.
CC   -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC   -!- SIMILARITY: BELONGS TO THE THYMIDINE/PYRIMIDINE-NUCLEOSIDE
CC       PHOSPHORYLASES FAMILY.
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CC   ----------------------------------------------------------------------
DR   EMBL; Z27121; CAA81645.1; -.
DR   HSSP; P77836; 1BRW.
DR   InterPro; IPR000312; Glycos_transf_3.
DR   InterPro; IPR000053; Thymid_phosphls.
DR   Pfam; PF00591; Glycos_transf_3; 1.
DR   ProDom; PD005916; Thymid_phosphls; 1.
DR   PROSITE; PS00647; THYMID_PHOSPHORYLASE; PARTIAL.
KW   Transferase; Glycosyltransferase.
FT   NON_TER      1      1
SQ   SEQUENCE   272 AA;  30411 MW;  B06BFB86FB6008EB CRC64;

  Query Match             44.5%;  Score 48.5;  DB 1;  Length 272;
  Best Local Similarity   48.0%;  Pred. No. 4.1;
  Matches   12;  Conservative    4;  Mismatches    6;  Indels    3;  Gaps    1;

Qy          1 GIGKFLK---KAKKFGKAFVKILKK 22
                | | |:|   :||| ||  ::| ||
Db         43 GNGAFMKDINEAKKLGKLMIEIGKK 67


RESULT 3
VP5_EHDV1
ID   VP5_EHDV1      STANDARD;      PRT;   527 AA.
AC   Q01175;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   Outer capsid protein VP5.
GN   S5.
OS   Epizootic hemorrhagic disease virus (serotype 1) (Ehdv-1).
OC   Viruses; dsRNA viruses; Reoviridae; Orbivirus.
OX   NCBI_TaxID=33720;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92116632; PubMed=1662845;
RA   Iwata H., Hirasawa T., Roy P.;
RT   "Complete nucleotide sequence of segment 5 of epizootic haemorrhagic
RT   disease virus; the outer capsid protein VP5 is homologous to the VP5
RT   protein of bluetongue virus.";
RL   Virus Res. 20:273-281(1991).
CC   -!- FUNCTION: THE VP5 PROTEIN IS ONE OF THE TWO PROTEINS (WITH VP2)
CC       WHICH CONSTITUTE THE VIRUS PARTICLE OUTER CAPSID.
CC   -!- SIMILARITY: BELONGS TO THE REOVIRUSES VP5 FAMILY.
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CC   ----------------------------------------------------------------------
DR   EMBL; X55782; CAA39303.1; -.
DR   PIR; S26752; S26752.
DR   PIR; S18762; S18762.
DR   InterPro; IPR000145; Orbi_VP5.
```

```
DR   Pfam; PF00901; Orbi_VP5; 1.
KW   Coat protein.
SQ   SEQUENCE   527 AA;  59119 MW;  8651D7346FBD3631 CRC64;

  Query Match             43.1%;  Score 47;  DB 1;  Length 527;
  Best Local Similarity   61.5%;  Pred. No. 13;
  Matches    8;  Conservative    3;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          2 IGKFLKKAKKFGK 14
              :|||:|:  ||||
Db          1 MGKFIKQLSKFGK 13


RESULT 4
Y053_METJA
ID   Y053_METJA     STANDARD;      PRT;   227 AA.
AC   Q60360;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Hypothetical protein MJ0053.
GN   MJ0053.
OS   Methanococcus jannaschii.
OC   Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC   Methanocaldococcaceae; Methanocaldococcus.
OX   NCBI_TaxID=2190;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX   MEDLINE=96337999; PubMed=8688087;
RA   Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA   Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA   Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA   Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA   Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA   Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA   Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA   Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT   "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT   jannaschii.";
RL   Science 273:1058-1073(1996).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; U67463; AAB98039.1; -.
DR   TIGR; MJ0053; -.
KW   Hypothetical protein; ATP-binding; Complete proteome.
FT   NP_BIND      17     24       ATP (POTENTIAL).
SQ   SEQUENCE   227 AA;  26722 MW;  A10A48D331225665 CRC64;

  Query Match             42.2%;  Score 46;  DB 1;  Length 227;
  Best Local Similarity   58.8%;  Pred. No. 8.2;
  Matches   10;  Conservative    3;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IGKFLKKAKKFGKAFVK 18
              | | ::||||| | |:
Db         68 INKEIEKAKKFGYAVVE 84


RESULT 5
TRI_PONLE
ID   TRI_PONLE      STANDARD;      PRT;   201 AA.
AC   P05547;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   01-NOV-1995 (Rel. 32, Last annotation update)
DE   Troponin I.
OS   Pontastacus leptodactylus (Narrow-fingered crayfish) (Astacus
OS   leptodactylus).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Crustacea;
OC   Malacostraca; Eumalacostraca; Eucarida; Decapoda; Pleocyemata;
OC   Astacidea; Astacoidea; Astacidae; Pontastacus.
OX   NCBI_TaxID=6717;
RN   [1]
RP   SEQUENCE.
RX   MEDLINE=89109165; PubMed=2912973;
RA   Kobayashi T., Takagi T., Konishi K., Cox J.A.;
RT   "Amino acid sequence of crayfish troponin I.";
RL   J. Biol. Chem. 264:1551-1557(1989).
CC   -!- FUNCTION: TROPONIN I IS THE ACTOMYOSIN ATPASE INHIBITORY SUBUNIT
CC       PRESENT IN THE THIN FILAMENT REGULATORY COMPLEX.
CC   -!- MISCELLANEOUS: THERE IS A 30 RESIDUE LONG N-TERMINAL TAIL THAT
CC       DOES NOT OCCUR IN SKELETAL MUSCLE TNI'S, BUT IS PRESENT IN CARDIAC
CC       MUSCLE TNI'S.
DR   PIR; A31484; A31484.
DR   InterPro; IPR001978; Troponin.
DR   Pfam; PF00992; Troponin; 1.
KW   Methylation; Actin-binding; Acetylation.
FT   MOD_RES       1      1       ACETYLATION (PROBABLE).
FT   MOD_RES     142    142       METHYLATION (TRI-).
FT   MOD_RES     146    146       METHYLATION (TRI-).
FT   DOMAIN      108    117       TROPONIN T-INTERACTION.
FT   DOMAIN      135    148       ACTIN-BINDING.
SQ   SEQUENCE   201 AA;  23490 MW;  47585EB56DB88A65 CRC64;

  Query Match             41.3%;  Score 45;  DB 1;  Length 201;
  Best Local Similarity   45.8%;  Pred. No. 10;
  Matches   11;  Conservative    2;  Mismatches    7;  Indels    4;  Gaps    1;

Qy          3 GKF----LKKAKKFGKAFVKILKK 22
              |||    |||  |:   | |: ||
Db        138 GKFIKPTLKKVSKYENKFAKLQKK 161


RESULT 6
TRI_DROME
ID   TRI_DROME      STANDARD;      PRT;   268 AA.
AC   P36188;
DT   01-JUN-1994 (Rel. 29, Created)
DT   15-JUN-2002 (Rel. 41, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Troponin I (TNI) (Wings apart-A protein) (Heldup protein).
GN   WUPA OR HDP OR TNI.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC   Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 2 AND 9), AND FUNCTION.
RC   STRAIN=Canton-S; TISSUE=Embryo, and Larva;
RX   MEDLINE=91115093; PubMed=1899228;
RA   Barbas J.A., Galceran J., Krah-Jentgens I., de la Pompa J.L.,
RA   Canal I., Pongs O., Ferrus A.;
RT   "Troponin I is encoded in the haplolethal region of the Shaker gene
RT   complex of Drosophila.";
RL   Genes Dev. 5:132-140(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Oregon-R;
RX   MEDLINE=91340840; PubMed=1908472;
RA   Beall C.J., Fyrberg E.;
RT   "Muscle abnormalities in Drosophila melanogaster heldup mutants are
RT   caused by missing or aberrant troponin-I isoforms.";
RL   J. Cell Biol. 114:941-951(1991).
RN   [3]
RP   ALTERNATIVE SPLICING, TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RX   MEDLINE=93180788; PubMed=7680094;
RA   Barbas J.A., Galceran J., Torroja L., Prado A., Ferrus A.;
RT   "Abnormal muscle development in the heldup3 mutant of Drosophila
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RT   melanogaster is caused by a splicing defect affecting selected
RT   troponin I isoforms.";
RL   Mol. Cell. Biol. 13:1433-1439(1993).
CC   -!- FUNCTION: Troponin I is the ATPase inhibitory subunit of Troponin
CC       in the thin filament regulatory complex. Involved in the
CC       development and maintenance of muscle and nervous system. May also
CC       be involved in the cytoskeletal apparatus.
CC   -!- ALTERNATIVE PRODUCTS: 10 isoforms; 1, 2, 3, 4, 5, 6, 7, 8, 9 and
CC       10 (shown here); are produced by alternative splicing. Exon 3 is
CC       either present or absent, exon 6 has 4 mutually exclusive forms
CC       (6a1, 6a2, 6b1 and 6b2) and C-terminal exons 9 and 10 are mutually
CC       exclusive.
CC   -!- TISSUE SPECIFICITY: All isoforms are expressed in somatic muscle.
CC       Isoforms containing exon 6a1 (isoforms 1 and 2) are expressed in
CC       all muscles but highest expression is in abdominal muscle and
CC       splanchnic muscle of the gut. Isoforms containing exon 6b1
CC       (isoforms 5, 6, 9 and 10) are highly expressed in the tergal
CC       depressor of trochanter (TDT) muscle.
CC   -!- DEVELOPMENTAL STAGE: Isoforms containing exon 3 (isoform 9 and
CC       isoform 10) are expressed in adults. Isoforms containing exon 6a1
CC       (isoforms 1 and 2) are expressed at all developmental stages.
CC       Isoforms containing exon 6a2 (isoforms 3 and 4) are weakly
CC       expressed in embryos and larvae and very weakly in adults.
CC       Isoforms containing exon 6b1 (isoforms 5, 6, 9 and 10) are weakly
CC       expressed in larva and increase during metamorphosis. Isoforms
CC       containing exon 6b2 (isoforms 7 and 8) are weakly expressed in
CC       embryos and larvae and at a higher level in adults.
CC   -!- MISCELLANEOUS: TROPONIN I BINDS TO ACTIN-TROPOMYOSIN.
CC   ----------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; X58188; CAA41171.1; -.
DR   EMBL; X59376; CAA42020.1; -.
DR   PIR; A38594; A38594.
DR   PIR; B38594; B38594.
DR   PIR; A40547; A40547.
DR   FlyBase; FBgn0004028; wupA.
DR   InterPro; IPR001978; Troponin.
DR   Pfam; PF00992; Troponin; 1.
KW   Muscle protein; Actin-binding; Acetylation; Methylation;
KW   Alternative splicing.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   MOD_RES       1      1       ACETYLATION (BY SIMILARITY).
FT   MOD_RES     200    200       METHYLATION (TRI-) (BY SIMILARITY).
FT   MOD_RES     204    204       METHYLATION (TRI-) (BY SIMILARITY).
FT   DOMAIN      161    170       TROPONIN T-INTERACTION (BY SIMILARITY).
FT   DOMAIN      188    201       ACTIN-BINDING (BY SIMILARITY).
FT   VARSPLIC      5     65       MISSING (IN ISOFORM 1, ISOFORM 2, ISOFORM
FT                                3, ISOFORM 4, ISOFORM 5, ISOFORM 6,
FT                                ISOFORM 7 AND ISOFORM 8).
FT   VARSPLIC    150    182       GELQEICEEYYERMYICEGQKWDLEYEVRKKDW -> DTLK
FT                                SLIKQHYDRINKLEDQKYDLEYVVKRKDV (IN ISOFORM
FT                                1 AND ISOFORM 2).
FT   VARSPLIC    150    182       GELQEICEEYYERMYICEGQKWDLEYEVRKKDW -> DTIQ
FT                                SVCKDYHSKILKLESEKYDFEYDVARKDY (IN ISOFORM
FT                                3 AND ISOFORM 4).
FT   VARSPLIC    150    182       GELQEICEEYYERMYICEGQKWDLEYEVRKKDW -> AELQ
FT                                TICKQYWQRVYSLEGDKFDLEHVQKVKAQ (IN ISOFORM
FT                                7 AND ISOFORM 8).
FT   VARSPLIC    248    268       PDWSKGKPGDAKVKEEVEAEA -> IKDAAVLNKAKK (IN
FT                                ISOFORM 1, ISOFORM 3, ISOFORM 5, ISOFORM
FT                                7 AND ISOFORM 9).
SQ   SEQUENCE   268 AA;  29950 MW;  16C121C96200906F CRC64;

  Query Match           41.3%;  Score 45;  DB 1;  Length 268;
  Best Local Similarity   45.8%;  Pred. No. 13;
  Matches   11;  Conservative    2;  Mismatches    7;  Indels    4;  Gaps    1;

Qy          3 GKF----LKKAKKFGKAFVKILKK 22
              |||    |||  |:   | |: ||
Db        196 GKFVKPALKKVSKYENKFAKLQKK 219


RESULT 7
P115_MYCGE
ID   P115_MYCGE     STANDARD;      PRT;   982 AA.
AC   P47540; Q49301;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   P115 protein homolog.
GN   MG298.
OS   Mycoplasma genitalium.
OC   Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX   NCBI_TaxID=2097;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 33530 / G-37;
RX   MEDLINE=96026346; PubMed=7569993;
RA   Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA   Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
RA   Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
RA   Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA   Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
RA   Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT   "The minimal gene complement of Mycoplasma genitalium.";
RL   Science 270:397-403(1995).
RN   [2]
RP   SEQUENCE OF 915-981 FROM N.A.
RC   STRAIN=ATCC 33530 / G-37;
RX   MEDLINE=94075230; PubMed=8253680;
RA   Peterson S.N., Hu P.-C., Bott K.F., Hutchison C.A. III;
RT   "A survey of the Mycoplasma genitalium genome by using random
RT   sequencing.";
RL   J. Bacteriol. 175:7918-7930(1993).
CC   -!- DOMAIN: CONSISTS OF TWO PUTATIVE CENTRAL COILED-COIL REGIONS
CC       FLANKED BY PUTATIVE GLOBULAR REGIONS AT THE N- AND C-TERMINUS.
CC   -!- SIMILARITY: BELONGS TO THE SMC FAMILY. SIMILAR TO OTHER MYCOPLASMA
CC       P115.
CC   ----------------------------------------------------------------------
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CC   ----------------------------------------------------------------------
DR   EMBL; U39710; AAC71520.1; -.
DR   EMBL; U02177; AAD12461.1; -.
DR   TIGR; MG298; -.
DR   InterPro; IPR003405; SMC_C.
DR   InterPro; IPR003395; SMC_N.
DR   Pfam; PF02463; SMC_N; 1.
DR   Pfam; PF02483; SMC_C; 1.
KW   Hypothetical protein; ATP-binding; Coiled coil; Complete proteome.
FT   NP_BIND      32     39       ATP (POTENTIAL).
FT   DOMAIN      174    232       COILED COIL (POTENTIAL).
FT   DOMAIN      264    383       COILED COIL (POTENTIAL).
FT   DOMAIN      573    835       COILED COIL (POTENTIAL).
FT   DOMAIN      955    982       COILED COIL (POTENTIAL).
FT   DOMAIN      884    912       ALA/ASP-RICH (DA-BOX).
FT   CONFLICT    975    981       YVSENDS -> ICIWKWF (IN REF. 2).
SQ   SEQUENCE   982 AA;  111073 MW;  E31CA2430B895A87 CRC64;

  Query Match           41.3%;  Score 45;  DB 1;  Length 982;
  Best Local Similarity   47.6%;  Pred. No. 45;
  Matches   10;  Conservative    4;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          2 IGKFLKKAKKFGKAFVKILKK 22
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                :| |||  |:: || :| | |.
Db        422 LGTFLKFDKQYEKAILKALGK 442


RESULT 8
DPO3_BACSU
ID   DPO3_BACSU     STANDARD;      PRT;  1437 AA.
AC   P13267;
DT   01-JAN-1990 (Rel. 13, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   DNA polymerase III polC-type (EC 2.7.7.7) (PolIII).
GN   POLC OR DNAF OR MUTI.
OS   Bacillus subtilis.
OC   Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX   NCBI_TaxID=1423;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   STRAIN=168 / BD541;
RX   MEDLINE=91192612; PubMed=1901559;
RA   Hammond R.A., Barnes M.H., Mack S.L., Mitchener J.A., Brown N.C.;
RT   "Bacillus subtilis DNA polymerase III: complete sequence,
RT   overexpression, and characterization of the polC gene.";
RL   Gene 98:29-36(1991).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=SB19;
RX   MEDLINE=89282784; PubMed=2499883;
RA   Sanjanwala B., Ganesan A.T.;
RT   "DNA polymerase III gene of Bacillus subtilis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:4421-4424(1989).
RN   [3]
RP   REVISIONS.
RX   MEDLINE=91246123; PubMed=1840638;
RA   Sanjanwala B., Ganesan A.T.;
RT   "Genetic structure and domains of DNA polymerase III of Bacillus
RT   subtilis.";
RL   Mol. Gen. Genet. 226:467-472(1991).
RN   [4]
RP   SEQUENCE OF 1-55 FROM N.A.
RC   STRAIN=SG64;
RX   MEDLINE=93173115; PubMed=7679775;
RA   Sanjanwala B., Ganesan A.T.;
RT   "Leader region of the gene encoding DNA polymerase III of Bacillus
RT   subtilis.";
RL   Mol. Gen. Genet. 236:374-378(1993).
RN   [5]
RP   SEQUENCE OF 1150-1229 FROM N.A.
RX   MEDLINE=90152360; PubMed=2515995;
RA   Barnes M.H., Hammond R.A., Foster K.A., Mitchener J.A., Brown N.C.;
RT   "The cloned polC gene of Bacillus subtilis: characterization of the
RT   azp12 mutation and controlled in vitro synthesis of active DNA
RT   polymerase III.";
RL   Gene 85:177-186(1989).
RN   [6]
RP   MUTAGENESIS.
RX   MEDLINE=92192477; PubMed=1312503;
RA   Barnes M.H., Hammond R.A., Kennedy C.S., Mack S.L., Brown N.C.;
RT   "Localization of the exonuclease and polymerase domains of Bacillus
RT   subtilis DNA polymerase III.";
RL   Gene 111:43-49(1992).
CC   -!- FUNCTION: REQUIRED FOR REPLICATIVE DNA SYNTHESIS. THIS DNA
CC       POLYMERASE ALSO EXHIBITS 3' TO 5' EXONUCLEASE ACTIVITY.
CC   -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC       + {DNA}(N).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- MISCELLANEOUS: MUTANT AZP12 HAS A FORM OF DNA POLYMERASE III
CC       RESISTANT TO HYDROXYPHENYLAZOPYRIMIDINES.
CC   -!- SIMILARITY: BELONGS TO THE DNA POLYMERASE TYPE-C FAMILY. POLC
CC       SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X52116; CAA36362.1; -.
DR   EMBL; M22996; AAA22666.1; -.
DR   EMBL; M33543; AAA22667.1; -.
DR   EMBL; S55653; -; NOT_ANNOTATED_CDS.
DR   EMBL; Z99112; CAB13531.1; -.
DR   PIR; A33920; A33920.
DR   PIR; JH0232; JH0232.
DR   PIR; S10459; S10459.
DR   SubtiList; BG10263; polC.
DR   InterPro; IPR000520; Exonuclease.
DR   InterPro; IPR004013; PHP_C.
DR   InterPro; IPR003141; PHP_N.
DR   InterPro; IPR004365; tRNA_anti.
DR   Pfam; PF00929; Exonuclease; 1.
DR   Pfam; PF01336; tRNA_anti; 1.
DR   Pfam; PF02231; PHP_N; 1.
DR   Pfam; PF02811; PHP_C; 1.
DR   SMART; SM00479; EXOIII; 1.
DR   SMART; SM00481; POLIIIAc; 1.
DR   TIGRFAMs; TIGR00573; dnaq; 1.
KW   Transferase; DNA-directed DNA polymerase; DNA replication; Hydrolase;
KW   Nuclease; Exonuclease; Antibiotic resistance; Complete proteome.
FT   DOMAIN      421    586       EXONUCLEASE.
FT   DOMAIN      613   1437       DNTP POLYMERIZATION SITE (POTENTIAL).
FT   DOMAIN     1393   1437       CONTAINS THE ACTIVE SITE OF THE
FT                                ENZYME.
FT   VARIANT    1175   1175       S -> A (IN MUTANT AZP12).
FT   MUTAGEN     427    427       E->A: DESTROYS BOTH POL & EXO ACTIVITIES.
FT   MUTAGEN     427    427       E->Q: DESTROYS EXO ACTIVITY; DECREASE POL
FT                                ACTIVITY.
FT   CONFLICT    184    188       EDQER -> KTKSW (IN REF. 2).
FT   CONFLICT    495    496       EW -> VR (IN REF. 2).
FT   CONFLICT    829    829       M -> S (IN REF. 2).
FT   CONFLICT   1015   1015       G -> E (IN REF. 2).
FT   CONFLICT   1190   1190       E -> D (IN REF. 2).
FT   CONFLICT   1405   1406       LQ -> FE (IN REF. 2).
SQ   SEQUENCE   1437 AA;  162662 MW;  0C04FC12D08C2E74 CRC64;

  Query Match             41.3%;  Score 45;  DB 1;  Length 1437;
  Best Local Similarity   61.5%;  Pred. No. 65;
  Matches    8;  Conservative    4;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFG 13
              |||| :::|||:|
Db        351 GIGKLVEQAKKWG 363


RESULT 9
FA39_HUMAN
ID   FA39_HUMAN     STANDARD;      PRT;   170 AA.
AC   P49913;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Antibacterial protein FALL-39 precursor (FALL-39 peptide antibiotic)
DE   (Antimicrobial protein CAP-18) (LL-37).
GN   CAMP OR FALL39 OR CAP18.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND SYNTHESIS OF 132-170.
RC   TISSUE=Bone marrow;
RX   MEDLINE=95116523; PubMed=7529412;
RA   Agerberth B., Gunne H., Odeberg J., Kogner P., Boman H.G.,
RA   Gudmundsson G.H.;
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RT   "FALL-39, a putative human peptide antibiotic, is cysteine-free and
RT   expressed in bone marrow and testis.";
RL   Proc. Natl. Acad. Sci. U.S.A. 92:195-199(1995).
RN   [2]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 42-68 AND 83-100.
RC   TISSUE=Bone marrow;
RX   MEDLINE=95339969; PubMed=7615076;
RA   Cowland J.B., Johnsen A.H., Borregaard N.;
RT   "hCAP-18, a cathelin/pro-bactenecin-like protein of human neutrophil
RT   specific granules.";
RL   FEBS Lett. 368:173-176(1995).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Bone marrow;
RX   MEDLINE=95197251; PubMed=7890387;
RA   Larrick J.W., Hirata M., Balint R.F., Lee J., Zhong J., Wright S.C.;
RT   "Human CAP18: a novel antimicrobial lipopolysaccharide-binding
RT   protein.";
RL   Infect. Immun. 63:1291-1297(1995).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97102716; PubMed=8946956;
RA   Larrick J.W., Lee J., Ma S., Li X., Francke U., Wright S.C.,
RA   Balint R.F.;
RT   "Structural, functional analysis and localization of the human CAP18
RT   gene.";
RL   FEBS Lett. 398:74-80(1996).
CC   -!- FUNCTION: BINDS TO BACTERIAL LIPOPOLYSACCHARIDES (LPS), HAS
CC       ANTIBACTERIAL ACTIVITY.
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN BONE MARROW AND TESTIS AND
CC       NEUTROPHILS.
CC   -!- PTM: THE N-TERMINUS IS BLOCKED.
CC   -!- SIMILARITY: BELONGS TO THE CATHELICIDIN FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; Z38026; CAA86115.1; -.
DR   EMBL; X89658; CAA61805.1; -.
DR   EMBL; U19970; AAA74084.1; -.
DR   EMBL; U48795; AAC02634.1; -.
DR   EMBL; X96735; -; NOT_ANNOTATED_CDS.
DR   Genew; HGNC:1472; CAMP.
DR   MIM; 600474; -.
DR   InterPro; IPR001894; Cathelicidin.
DR   Pfam; PF00666; Cathelicidins; 1.
DR   ProDom; PD001838; Cathelicidin; 1.
DR   PROSITE; PS00946; CATHELICIDINS_1; 1.
DR   PROSITE; PS00947; CATHELICIDINS_2; 1.
KW   Antibiotic; Signal.
FT   SIGNAL        1     30       POTENTIAL.
FT   PROPEP       31    131
FT   CHAIN       132    170       ANTIBACTERIAL PROTEIN FALL-39.
FT   CHAIN       134    170       ANTIBACTERIAL PROTEIN LL-37.
FT   MOD_RES      31     31       PYRROLIDONE CARBOXYLIC ACID (BY
FT                                SIMILARITY).
FT   DISULFID     86     97       BY SIMILARITY.
FT   DISULFID    108    125       BY SIMILARITY.
FT   CONFLICT      6      6       D -> N (IN REF. 1).
SQ   SEQUENCE   170 AA;  19301 MW;  055B07DCA95A7D16 CRC64;

  Query Match             40.8%;  Score 44.5;  DB 1;  Length 170;
  Best Local Similarity   40.9%;  Pred. No. 10;
  Matches    9;  Conservative    7;  Mismatches    5;  Indels    1;  Gaps    1;

Qy          2 IGKFLKKAK-KFGKAFVKILKK 22
              :| | :|:| | || | :|:::
Db        135 LGDFFRKSKEKIGKEFKRIVQR 156
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RESULT 10
PO14_NASVI
ID   PO14_NASVI     STANDARD;      PRT;   392 AA.
AC   Q03272;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Retrovirus-related POL polyprotein from type I retrotransposable
DE   element R1 [Contains: Reverse transcriptase (EC 2.7.7.49);
DE   Endonuclease] (Fragment).
OS   Nasonia vitripennis (Parasitic wasp).
OC   Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC   Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita;
OC   Chalcidoidea; Pteromalidae; Nasonia.
OX   NCBI_TaxID=7425;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93196484; PubMed=8383793;
RA   Burke W.D., Eickbush D.G., Xiong Y., Jakubczak J.L., Eickbush T.H.;
RT   "Sequence relationship of retrotransposable elements R1 and R2 within
RT   and between divergent insect species.";
RL   Mol. Biol. Evol. 10:163-185(1993).
CC   -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC       + {DNA}(N).
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; L00943; AAA30340.1; -.
DR   PIR; E44490; E44490.
DR   InterPro; IPR000477; RVTse.
DR   Pfam; PF00078; rvt; 1.
KW   Transferase; RNA-directed DNA polymerase; Transposable element;
KW   Hydrolase; Nuclease; Endonuclease.
FT   NON_TER       1      1
FT   DOMAIN       <1    230       REVERSE TRANSCRIPTASE.
FT   DOMAIN      231    392       NUCLEIC ACID-BINDING ENDONUCLEASE.
SQ   SEQUENCE   392 AA;  43758 MW;  D644BD53EDAD77F6 CRC64;

  Query Match             40.4%;  Score 44;  DB 1;  Length 392;
  Best Local Similarity   47.6%;  Pred. No. 27;
  Matches   10;  Conservative    3;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          2 IGKFLKKAKKFGKAFVKILKK 22
              :| |:|| |  |   ||| :|
Db         46 VGIFVKKPKVVGSKAVKINRK 66


RESULT 11
PHYB_ASPAW
ID   PHYB_ASPAW     STANDARD;      PRT;   479 AA.
AC   P34755;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   30-MAY-2000 (Rel. 39, Last annotation update)
DE   3-phytase B precursor (EC 3.1.3.8) (Myo-inositol-hexaphosphate
DE   3-phosphohydrolase B) (pH 2.5 optimum acid phosphatase).
GN   PHYB OR APH.
OS   Aspergillus awamori.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX   NCBI_TaxID=105351;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ALK0243;
RX   MEDLINE=94040796; PubMed=8224894;
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RA   Piddington C.S., Houston C.S., Paloheimo M.T., Cantrell M.A.,
RA   Miettinen-Oinonen A., Nevalainen H., Rambosek J.A.;
RT   "The cloning and sequencing of the genes encoding phytase (phy) and
RT   pH 2.5-optimum acid phosphatase (aph) from Aspergillus niger var.
RT   awamori.";
RL   Gene 133:55-62(1993).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX   MEDLINE=99264417; PubMed=10329192;
RA   Kostrewa D., Wyss M., D'Arcy A., van Loon A.P.;
RT   "Crystal structure of Aspergillus niger pH 2.5 acid phosphatase at
RT   2.4-A resolution.";
RL   J. Mol. Biol. 288:965-974(1999).
CC   -!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
CC       FROM PHYTATE.
CC   -!- CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate + H(2)O = D-myo-
CC       inositol 1,2,4,5,6-pentakisphosphate + phosphate.
CC   -!- SUBUNIT: HOMODIMER.
CC   -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L02420; AAA16897.1; -.
DR   PIR; JN0890; JN0890.
DR   PDB; 1QFX; 19-APR-00.
DR   InterPro; IPR000560; HisAc_phsphtse.
DR   Pfam; PF00328; acid_phosphat; 1.
DR   PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR   PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW   Hydrolase; Glycoprotein; Signal; 3D-structure.
FT   SIGNAL       1     19       BY SIMILARITY.
FT   CHAIN       20    479       3-PHYTASE B.
FT   ACT_SITE    82     82       NUCLEOPHILIC ACCEPTOR.
FT   ACT_SITE   337    337       PROTON DONOR.
FT   DISULFID    71    387
FT   DISULFID   128    472
FT   DISULFID   216    441
FT   DISULFID   225    298
FT   DISULFID   413    421
FT   CARBOHYD   191    191       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   315    315       N-LINKED (GLCNAC. . .).
FT   CARBOHYD   458    458       N-LINKED (GLCNAC. . .).
SQ   SEQUENCE   479 AA;  52678 MW;  4F8E0F3778CC3B08 CRC64;

  Query Match          40.4%;  Score 44;  DB 1;  Length 479;
  Best Local Similarity  43.8%;  Pred. No. 33;
  Matches    7;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAF 16
              | |: :: |:|||: |
Db        172 GYGRVIETARKFGEGF 187


RESULT 12
PHYB_ASPNG
ID   PHYB_ASPNG     STANDARD;      PRT;   479 AA.
AC   P34754;
DT   01-FEB-1994 (Rel. 28, Created)
DT   01-FEB-1994 (Rel. 28, Last sequence update)
DT   01-JUN-1994 (Rel. 29, Last annotation update)
DE   3-phytase B precursor (EC 3.1.3.8) (Myo-inositol-hexaphosphate
DE   3-phosphohydrolase B) (3 phytase B) (Myo-inositol hexakisphosphate
DE   phosphohydrolase B).
GN   PHYB.
OS   Aspergillus niger.
OC   Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC   Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX   NCBI_TaxID=5061;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 20-101; 133-141 AND 376-399.
RX   MEDLINE=93371452; PubMed=7916610;
RA   Ehrlich K.C., Montalbano B.G., Mullaney E.J., Dischinger H.C. Jr.,
RA   Ullah A.H.J.;
RT   "Identification and cloning of a second phytase gene (phyB) from
RT   Aspergillus niger (ficuum).";
RL   Biochem. Biophys. Res. Commun. 195:53-57(1993).
CC   -!- FUNCTION: CATALYZES THE HYDROLYSIS OF INORGANIC ORTHOPHOSPHATE
CC       FROM PHYTATE.
CC   -!- CATALYTIC ACTIVITY: Myo-inositol hexakisphosphate + H(2)O = D-myo-
CC       inositol 1,2,4,5,6-pentakisphosphate + phosphate.
CC   -!- SIMILARITY: BELONGS TO THE HISTIDINE ACID PHOSPHATASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L20567; AAA02934.1; -.
DR   HSSP; P34755; 1QFX.
DR   InterPro; IPR000560; HisAc_phsphtse.
DR   Pfam; PF00328; acid_phosphat; 1.
DR   PROSITE; PS00616; HIS_ACID_PHOSPHAT_1; 1.
DR   PROSITE; PS00778; HIS_ACID_PHOSPHAT_2; 1.
KW   Hydrolase; Glycoprotein; Signal.
FT   SIGNAL       1     19
FT   CHAIN       20    479       3-PHYTASE B.
FT   ACT_SITE    81     81       REQUIRED FOR BINDING SUBSTRATE
FT                               (BY SIMILARITY).
FT   ACT_SITE    82     82       NUCLEOPHILIC ACCEPTOR (BY SIMILARITY).
FT   ACT_SITE   337    337       PROTON DONOR (BY SIMILARITY).
FT   CARBOHYD   106    106       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   191    191       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   227    227       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   250    250       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   315    315       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   425    425       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   442    442       N-LINKED (GLCNAC. . .) (POTENTIAL).
FT   CARBOHYD   458    458       N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ   SEQUENCE   479 AA;  52611 MW;  395D4DA2B50FDFC4 CRC64;

  Query Match          40.4%;  Score 44;  DB 1;  Length 479;
  Best Local Similarity  43.8%;  Pred. No. 33;
  Matches    7;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAF 16
              | |: :: |:|||: |
Db        172 GYGRVIETARKFGEGF 187


RESULT 13
IF3C_EUGGR
ID   IF3C_EUGGR     STANDARD;      PRT;   538 AA.
AC   P36177;
DT   01-JUN-1994 (Rel. 29, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   Translation initiation factor IF-3, chloroplast precursor (IF-3CHL).
OS   Euglena gracilis.
OC   Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
OX   NCBI_TaxID=3039;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   STRAIN=B;
RX   MEDLINE=94193615; PubMed=8144528;
RA   Lin Q., Ma L., Burkhart W., Spremulli L.L.;
RT   "Isolation and characterization of cDNA clones for chloroplast
RT   translational initiation factor-3 from Euglena gracilis.";
```

```
RL   J. Biol. Chem. 269:9436-9444(1994).
CC   -!- FUNCTION: INVOLVED IN CHLOROPLAST PROTEIN SYNTHESIS. IT ENHANCES
CC       THE POLY(A,U,G)-DEPENDENT BINDING OF THE INITIATOR TRNA TO
CC       CHLOROPLAST 30S SUBUNITS.
CC   -!- SUBUNIT: MONOMER.
CC   -!- SUBCELLULAR LOCATION: Chloroplast.
CC   -!- PTM: THE N-TERMINUS IS BLOCKED.
CC   -!- SIMILARITY: BELONGS TO THE IF-3 FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; L23760; AAA20996.1; -.
DR   HSSP; P03000; 1TIF.
DR   InterPro; IPR001288; IF3.
DR   Pfam; PF00707; IF3; 1.
DR   ProDom; PD002880; IF3; 1.
DR   TIGRFAMs; TIGR00168; infC; 1.
DR   PROSITE; PS00938; IF3; 1.
KW   Initiation factor; Protein biosynthesis; Chloroplast; Transit peptide.
FT   TRANSIT       1   ?140       CHLOROPLAST (POTENTIAL).
FT   CHAIN      ?141    538       TRANSLATION INITIATION FACTOR IF-3.
FT   DOMAIN      141    290       HEAD.
FT   DOMAIN      291    474       IF-3 LIKE.
FT   DOMAIN      475    538       ASP/GLU-RICH (ACIDIC TAIL).
SQ   SEQUENCE   538 AA;  58254 MW;  F92B0881839B03E0 CRC64;

  Query Match             40.4%;  Score 44;  DB 1;  Length 538;
  Best Local Similarity   55.6%;  Pred. No. 36;
  Matches   10;  Conservative.   1;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFVK 18
              |:|  | | | ||| | |
Db        256 GLGLGLGKGKGFGKGFGK 273


RESULT 14
YGG8_YEAST
ID   YGG8_YEAST     STANDARD;      PRT;   194 AA.
AC   P53163;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   Putative 60S ribosomal protein L7/L12 homolog, mitochondrial
DE   precursor.
GN   YGL068W.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxID=4932;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=S288c;
RX   MEDLINE=97435481; PubMed=9290212;
RA   Rieger M., Brueckner M., Schaefer M., Mueller-Auer S.;
RT   "Sequence analysis of 203 kilobases from Saccharomyces cerevisiae
RT   chromosome VII.";
RL   Yeast 13:1077-1090(1997).
CC   -!- SUBCELLULAR LOCATION: Mitochondrial (Potential).
CC   -!- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; Z72591; CAA96773.1; -.
DR   HSSP; P02392; 1CTF.
DR   SGD; S0003036; YGL068W.
DR   InterPro; IPR000206; Ribosomal_L12.
DR   Pfam; PF00542; Ribosomal_L12; 1.
DR   ProDom; PD001326; Ribosomal_L12; 1.
KW   Hypothetical protein; Ribosomal protein; Mitochondrion;
KW   Transit peptide.
FT   TRANSIT       1      ?       MITOCHONDRION (POTENTIAL).
FT   CHAIN         ?    194       PUTATIVE 60S RIBOSOMAL PROTEIN L7/L12
FT                               HOMOLOG.
SQ   SEQUENCE   194 AA;  20650 MW;  D7892681B778B8A9 CRC64;

  Query Match             39.4%;  Score 43;  DB 1;  Length 194;
  Best Local Similarity   47.6%;  Pred. No. 20;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 IGKFLKKAKKFGKAFVKILKK 22
              :|  | :|||| :|  |:||:
Db        150 LGLSLVEAKKFVEAAPKVLKE 170


RESULT 15
ARCX_MYCPN
ID   ARCX_MYCPN     STANDARD;      PRT;   438 AA.
AC   P75218;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   16-OCT-2001 (Rel. 40, Last annotation update)
DE   Arginine deiminase-like protein.
GN   MPN560 OR MP282.
OS   Mycoplasma pneumoniae.
OC   Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX   NCBI_TaxID=2104;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 29342 / M129;
RX   MEDLINE=97105885; PubMed=8948633;
RA   Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
RA   Herrmann R.;
RT   "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT   pneumoniae.";
RL   Nucleic Acids Res. 24:4420-4449(1996).
CC   -!- SIMILARITY: BELONGS TO THE ARGININE DEIMINASE FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE000027; AAB95930.1; -.
DR   InterPro; IPR003876; Arg_deiminase.
DR   Pfam; PF02726; Arg_deiminase; 1.
KW   Hypothetical protein; Hydrolase; Complete proteome.
SQ   SEQUENCE   438 AA;  49442 MW;  E3DB589827675010 CRC64;

  Query Match             39.4%;  Score 43;  DB 1;  Length 438;
  Best Local Similarity   36.4%;  Pred. No. 42;
  Matches    8;  Conservative    8;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKAFVKILKK 22
              |   :|::|:|  : |:|||::
Db         65 GSAMYLERAQKEHQLFIKILRQ 86


Search completed: June 30, 2003, 16:08:08
Job time : 24 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: June 30, 2003, 16:05:14 ; Search time 29 Seconds
(without alignments)
156.312 Million cell updates/sec

Title: US-09-904-753-4
Perfect score: 109
Sequence: 1 GIGKFLKKAKKFGKAFVKILKK 22

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_21:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	53	48.6	787	17	Q9UYH2	Q9uyh2 pyrococcus
2	48	44.0	129	16	Q9KVR5	Q9kvr5 vibrio chol
3	48	44.0	142	4	Q9H642	Q9h642 homo sapien
4	47	43.1	179	17	Q8TQ97	Q8tq97 methanosarc
5	47	43.1	226	17	Q97ZG4	Q97zg4 sulfolobus
6	47	43.1	534	17	Q8ZWJ6	Q8zwj6 pyrobaculum
7	46	42.2	276	16	Q98PQ1	Q98pq1 mycoplasma
8	46	42.2	402	4	Q9H6S5	Q9h6s5 homo sapien
9	46	42.2	409	4	Q9UFT1	Q9uft1 homo sapien
10	46	42.2	462	16	Q8Z0W7	Q8z0w7 salmonella
11	46	42.2	1466	13	Q98TR8	Q98tr8 bufo bufo (
12	46	42.2	1963	5	Q9VSK5	Q9vsk5 drosophila
13	46	42.2	1966	5	Q9NHX6	Q9nhx6 drosophila
14	46	42.2	1985	5	Q8T9N4	Q8t9n4 drosophila
15	45.5	41.7	3933	5	O97239	O97239 plasmodium
16	45	41.3	179	16	Q8ZJ76	Q8zj76 yersinia pe
17	45	41.3	228	17	Q971V0	Q971v0 sulfolobus
18	45	41.3	271	5	Q9VWY4	Q9vwy4 drosophila
19	45	41.3	271	5	Q9VWY2	Q9vwy2 drosophila
20	45	41.3	318	5	Q9VWY3	Q9vwy3 drosophila
21	45	41.3	381	17	Q9HJ07	Q9hj07 thermoplasm
22	45	41.3	432	2	Q49134	Q49134 methylobact
23	45	41.3	627	17	O28241	O28241 archaeoglob
24	45	41.3	810	10	Q9AWY6	Q9awy6 oryza sativ
25	45	41.3	897	16	Q98QG9	Q98qg9 mycoplasma
26	45	41.3	1039	17	Q9YF27	Q9yf27 aeropyrum p
27	45	41.3	1080	17	Q8TWY2	Q8twy2 methanopyru
28	45	41.3	2269	5	Q26223	Q26223 plasmodium
29	45	41.3	2747	5	Q9BJX9	Q9bjx9 plasmodium
30	45	41.3	3151	5	Q8SR52	Q8sr52 encephalito
31	44.5	40.8	379	17	O29118	O29118 archaeoglob
32	44	40.4	68	16	Q8RFF7	Q8rff7 fusobacteri
33	44	40.4	156	16	Q927G8	Q927g8 listeria in
34	44	40.4	156	16	Q8Y405	Q8y405 listeria mo
35	44	40.4	343	16	O67374	O67374 aquifex aeo
36	44	40.4	389	17	Q97AK0	Q97ak0 thermoplasm
37	44	40.4	724	16	Q8XNJ0	Q8xnj0 clostridium
38	44	40.4	1607	16	Q8RH77	Q8rh77 fusobacteri
39	43.5	39.9	741	16	Q8RFF8	Q8rff8 fusobacteri
40	43	39.4	71	2	Q9AKJ1	Q9akj1 rickettsia
41	43	39.4	71	2	Q9AKP4	Q9akp4 rickettsia
42	43	39.4	75	16	Q92H63	Q92h63 rickettsia
43	43	39.4	168	2	Q936G8	Q936g8 staphylococ
44	43	39.4	191	2	P94239	P94239 borrelia bu
45	43	39.4	193	17	Q96YS4	Q96ys4 sulfolobus

ALIGNMENTS

RESULT 1
Q9UYH2
ID Q9UYH2 PRELIMINARY; PRT; 787 AA.
AC Q9UYH2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta-galactosidase (EC 3.2.1.23) (Lactase).
GN PAB1349.
OS Pyrococcus abyssi.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=29292;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ORSAY;
RA Heilig R.;
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome
RT structure and evolution.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AJ248287; CAB50440.1; -.
DR InterPro; IPR001944; GH_35.
DR InterPro; IPR003476; Glyco_hydro_42.
DR Pfam; PF01301; Glyco_hydro_35; 1.
DR Pfam; PF02449; Glyco_hydro_42; 1.
DR PRINTS; PR00742; GLHYDRLASE35.
KW Complete proteome.
SQ SEQUENCE 787 AA; 91778 MW; 1D37BE2847B3F8CA CRC64;

Query Match 48.6%; Score 53; DB 17; Length 787;
Best Local Similarity 64.7%; Pred. No. 15;
Matches 11; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

```
Qy          2 IGKFLKKAKKFGKAFVK 18
              |||||:  | |||: ||
Db        422 IGKFLRSNKDFGKSEVK 438
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RESULT 2

```
Q9KVR5
ID   Q9KVR5      PRELIMINARY;      PRT;   129 AA.
AC   Q9KVR5;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical protein VC0074.
GN   VC0074.
OS   Vibrio cholerae.
OC   Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX   NCBI_TaxID=666;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=EL TOR N16961 / SEROTYPE O1;
RX   MEDLINE=20406833; PubMed=10952301;
RA   Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA   Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA   Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA   Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA   McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA   Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA   Fraser C.M.;
RT   "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT   cholerae.";
RL   Nature 406:477-483(2000).
DR   EMBL; AE004098; AAF93252.1; -.
DR   TIGR; VC0074; -.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   129 AA;  14335 MW;  BA06D715CB328B63 CRC64;

  Query Match             44.0%;  Score 48;  DB 16;  Length 129;
  Best Local Similarity   58.8%;  Pred. No. 14;
  Matches   10;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          6 LKKAKKFGKAFVKILKK 22
              ||| :|| |   |:|||
Db         80 LKKQRKFHKKLEKVLKK 96


RESULT 3
Q9H642
ID   Q9H642      PRELIMINARY;      PRT;   142 AA.
AC   Q9H642;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   CDNA: FLJ22622 fis, clone HSI05669.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=SMALL INTESTINE;
RA   Watanabe K., Kumagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
RA   Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T.,
RA   Nakamura Y., Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AK026275; BAB15424.1; -.
DR   InterPro; IPR000008; C2.
DR   Pfam; PF00168; C2; 1.
DR   SMART; SM00239; C2; 1.
DR   PROSITE; PS50004; C2_DOMAIN_2; 1.
SQ   SEQUENCE   142 AA;  15304 MW;  6C070166F8160FDF CRC64;

  Query Match             44.0%;  Score 48;  DB 4;  Length 142;
  Best Local Similarity   40.0%;  Pred. No. 16;
  Matches   12;  Conservative    4;  Mismatches    6;  Indels    8;  Gaps    1;

Qy          1 GIGKFLKKAK--------KFGKAFVKILKK 22
              |: ||| :|:         ||:| | |||
Db         99 GLDKFLGRAEVDLRDLHSSLGKSFFKTLKK 128


RESULT 4
Q8TQ97
ID   Q8TQ97      PRELIMINARY;      PRT;   179 AA.
AC   Q8TQ97;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Intracellular protease.
GN   PFPI OR MA1654.
OS   Methanosarcina acetivorans.
OC   Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC   Methanosarcinaceae; Methanosarcina.
OX   NCBI_TaxID=2214;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C2A / ATCC 35395 / DSM 2834;
RX   MEDLINE=21929760; PubMed=11932238;
RA   Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA   FitzHugh W., Calvo S., Engels R., Smirnov S., Atnoor D., Brown A.,
RA   Allen N., Naylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA   Linton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA   Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA   Hedderich R., Ingram-Smith C., Kuettner H.C., Krzycki J.A.,
RA   Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA   Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA   Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA   Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA   Metcalf W.W., Birren B.;
RT   "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT   and physiological diversity.";
RL   Genome Res. 12:532-542(2002).
DR   EMBL; AE010838; AAM05062.1; -.
KW   Protease; Complete proteome.
SQ   SEQUENCE   179 AA;  19359 MW;  E0FDC30D4BF4F456 CRC64;

  Query Match             43.1%;  Score 47;  DB 17;  Length 179;
  Best Local Similarity   50.0%;  Pred. No. 28;
  Matches   10;  Conservative    4;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          3 GKFLKKAKKFGKAFVKILKK 22
              |:  : |: |||| :| |||
Db        159 GRDPRSAEAFGKAVLKALKK 178


RESULT 5
Q97ZG4
ID   Q97ZG4      PRELIMINARY;      PRT;   226 AA.
AC   Q97ZG4;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Hypothetical protein SSO0954.
GN   SSO0954.
OS   Sulfolobus solfataricus.
OC   Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
OC   Sulfolobus.
OX   NCBI_TaxID=2287;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 35092 / DSM 1617 / P2;
RX   MEDLINE=21332296; PubMed=11427726;
RA   She Q., Singh R.K., Confalonieri F., Zivanovic Y., Allard G.,
RA   Awayez M.J., Chan-Weiher C.C.-Y., Clausen I.G., Curtis B.A.,
RA   De Moors A., Erauso G., Fletcher C., Gordon P.M.K.,
RA   Heikamp-de Jong I., Jeffries A.C., Kozera C.J., Medina N., Peng X.,
RA   Thi-Ngoc H.P., Redder P., Schenk M.E., Theriault C., Tolstrup N.,
RA   Charlebois R.L., Doolittle W.F., Duguet M., Gaasterland T.,
RA   Garrett R.A., Ragan M.A., Sensen C.W., Van der Oost J.;
RT   "The complete genome of the crenarchaeon Sulfolobus solfataricus P2.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:7835-7840(2001).
DR   EMBL; AE006715; AAK41228.1; -.
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DR   InterPro; IPR004820; Cytidylyltransf.
DR   InterPro; IPR004821; Cyt_tran_rel.
DR   Pfam; PF01467; Cytidylyltransf; 1.
DR   TIGRFAMs; TIGR00125; cyt_tran_rel; 1.
KW   Hypothetical protein; Complete proteome.
SQ   SEQUENCE   226 AA;  26289 MW;  CF5CFD38B0BC0CE6 CRC64;

  Query Match             43.1%;  Score 47;  DB 17;  Length 226;
  Best Local Similarity   38.9%;  Pred. No. 35;
  Matches    7;  Conservative    7;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          4 KFLKKAKKFGKAFVKILK 21
              :|||:| |:|: :| : :
Db         99 EFLKEASKYGRVYVTVAR 116


RESULT 6
Q8ZWJ6
ID   Q8ZWJ6      PRELIMINARY;      PRT;   534 AA.
AC   Q8ZWJ6;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Iron-sulfur binding reductase, probable.
GN   PAE1762.
OS   Pyrobaculum aerophilum.
OC   Archaea; Crenarchaeota; Thermoprotei; Thermoproteales;
OC   Thermoproteaceae; Pyrobaculum.
OX   NCBI_TaxID=13773;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=IM2 / ATCC 51768 / DSM 7523;
RX   PubMed=11792869;
RA   Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,
RA   Miller J.H.;
RT   "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT   aerophilum.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
DR   EMBL; AE009838; AAL63706.1; -.
DR   InterPro; IPR001450; 4Fe4S_ferredoxin.
DR   InterPro; IPR004017; DUF224.
DR   Pfam; PF02754; DUF224; 2.
DR   PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
KW   Complete proteome.
SQ   SEQUENCE   534 AA;  59913 MW;  3F6AC627DD008440 CRC64;

  Query Match             43.1%;  Score 47;  DB 17;  Length 534;
  Best Local Similarity   47.6%;  Pred. No. 80;
  Matches   10;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          2 IGKFLKKAKKFGKAFVKILKK 22
              :| |  : ::  ||||:||||
Db        306 MGSFDGRTREIVKAFVEILKK 326


RESULT 7
Q98PQ1
ID   Q98PQ1      PRELIMINARY;      PRT;   276 AA.
AC   Q98PQ1;
DT   01-OCT-2001 (TrEMBLrel. 18, Created)
DT   01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Lipoprotein signal peptidase (Prolipoprotein signal peptidase) (Signal
DE   peptidase II)(SPase II) (EC 3.4.23.36).
GN   MYPU_6680.
OS   Mycoplasma pulmonis.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC   Mycoplasmataceae; Mycoplasma.
OX   NCBI_TaxID=2107;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=UAB CTIP;
RX   MEDLINE=21267165; PubMed=11353084;
RA   Chambaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
RA   Moszer I., Dybvig K., Wroblewski H., Viari A., Rocha E.P.C.,
RA   Blanchard A.;
RT   "The complete genome sequence of the murine respiratory pathogen
RT   Mycoplasma pulmonis.";
RL   Nucleic Acids Res. 29:2145-2153(2001).
DR   EMBL; AL445565; CAC13841.1; -.
DR   MypuList; MYPU_6680; -.
DR   InterPro; IPR001872; SigPTase_A8.
DR   PRINTS; PR00781; LIPOSIGPTASE.
KW   Hydrolase; Complete proteome.
SQ   SEQUENCE   276 AA;  31358 MW;  0AAFD091D28A5B1F CRC64;

  Query Match             42.2%;  Score 46;  DB 16;  Length 276;
  Best Local Similarity   69.2%;  Pred. No. 59;
  Matches    9;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          4 KFLKKAKKFGKAF 16
              ||: ||| | |||
Db         26 KFIVKAKSFSKAF 38


RESULT 8
Q9H6S5
ID   Q9H6S5      PRELIMINARY;      PRT;   402 AA.
AC   Q9H6S5;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   CDNA: FLJ21932 fis, clone HEP04318 (Unknown) (Protein for MGC:19467)
DE   (Protein for MGC:14416).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
RA   Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,
RA   Tanaka T., Nakamura Y., Isogai T., Sugano S.;
RT   "NEDO human cDNA sequencing project.";
RL   Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=MUSCLE;
RA   Strausberg R.;
RL   Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=UTERUS;
RA   Strausberg R.;
RL   Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + L-AMINO ACID + TRNA(AMINO ACID) = AMP +
CC       DIPHOSPHATE + L-AMINOACYL-TRNA(AMINO ACID).
CC   -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
DR   EMBL; AK025585; BAB15178.1; -.
DR   EMBL; BC011758; AAH11758.1; -.
DR   EMBL; BC007956; AAH07956.1; -.
DR   InterPro; IPR002106; AAtRNA_ligaseII.
DR   InterPro; IPR004154; HGTP_anticodon.
DR   InterPro; IPR002314; tRNA-synt_2b.
DR   InterPro; IPR002315; tRNA-synt_gly.
DR   InterPro; IPR002316; tRNA-synt_pro.
DR   Pfam; PF03129; HGTP_anticodon; 1.
DR   Pfam; PF00587; tRNA-synt_2b; 1.
DR   PRINTS; PR01043; TRNASYNTHGLY.
DR   PRINTS; PR01046; TRNASYNTHPRO.
DR   PROSITE; PS00179; AA_TRNA_LIGASE_II_1; 1.
KW   ATP-binding; Aminoacyl-tRNA synthetase; Ligase; Protein biosynthesis.
SQ   SEQUENCE   402 AA;  44842 MW;  36CF5BDC4C2365B3 CRC64;

  Query Match             42.2%;  Score 46;  DB 4;  Length 402;
  Best Local Similarity   57.1%;  Pred. No. 85;
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  Matches   12;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          2 IGKFLKKAKKFGKAFVKILKK 22
              ||  || | |||  || |  |
Db        345 IGNRLKDANKFGYPFVIIAGK 365


RESULT 9
Q9UFT1
ID   Q9UFT1      PRELIMINARY;      PRT;   409 AA.
AC   Q9UFT1;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE   Hypothetical 45.7 kDa protein (Fragment).
GN   DKFZP727A071.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BREAST CANCER;
RA   Poustka A., Klein M., Mewes H.W., Gassenhuber J., Wiemann S.;
RL   Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: ATP + L-AMINO ACID + TRNA(AMINO ACID) = AMP +
CC       DIPHOSPHATE + L-AMINOACYL-TRNA(AMINO ACID).
CC   -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
DR   EMBL; AL117473; CAB55948.1; -.
DR   InterPro; IPR002106; AAtRNA_ligaseII.
DR   InterPro; IPR004154; HGTP_anticodon.
DR   InterPro; IPR002314; tRNA-synt_2b.
DR   InterPro; IPR002315; tRNA-synt_gly.
DR   InterPro; IPR002316; tRNA-synt_pro.
DR   Pfam; PF03129; HGTP_anticodon; 1.
DR   Pfam; PF00587; tRNA-synt_2b; 1.
DR   PRINTS; PR01043; TRNASYNTHGLY.
DR   PRINTS; PR01046; TRNASYNTHPRO.
DR   PROSITE; PS00179; AA_TRNA_LIGASE_II_1; 1.
KW   ATP-binding; Aminoacyl-tRNA synthetase; Hypothetical protein; Ligase;
KW   Protein biosynthesis.
FT   NON_TER       1      1
SQ   SEQUENCE   409 AA;  45658 MW;  FAE58B08628B9FC5 CRC64;

  Query Match             42.2%;  Score 46;  DB 4;  Length 409;
  Best Local Similarity   57.1%;  Pred. No. 86;
  Matches   12;  Conservative    0;  Mismatches    9;  Indels    0;  Gaps    0;

Qy          2 IGKFLKKAKKFGKAFVKILKK 22
              ||  || | |||  || |  |
Db        352 IGNRLKDANKFGYPFVIIAGK 372


RESULT 10
Q8Z0W7
ID   Q8Z0W7      PRELIMINARY;      PRT;   462 AA.
AC   Q8Z0W7;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Subunit S of type I restriction-modification system.
GN   HSDS OR STY4881.
OS   Salmonella typhi.
OC   Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC   Salmonella.
OX   NCBI_TaxID=601;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CT18;
RX   MEDLINE=21534947; PubMed=11677608;
RA   Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA   Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA   Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA   Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA   Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA   Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA   Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA   Whitehead S., Barrell B.G.;
RT   "Complete genome sequence of a multiple drug resistant Salmonella
RT   enterica serovar Typhi CT18.";
RL   Nature 413:848-852(2001).
DR   EMBL; AL627284; CAD03369.1; -.
DR   InterPro; IPR000055; Methylase_S.
DR   Pfam; PF01420; Methylase_S; 2.
KW   Complete proteome.
SQ   SEQUENCE   462 AA;  51854 MW;  12C2151BCBA84178 CRC64;

  Query Match             42.2%;  Score 46;  DB 16;  Length 462;
  Best Local Similarity   64.3%;  Pred. No. 97;
  Matches    9;  Conservative    1;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          2 IGKFLKKAKKFGKA 15
              :|| | ||| || |
Db        239 LGKMLDKAKNFGSA 252


RESULT 11
Q98TR8
ID   Q98TR8      PRELIMINARY;      PRT;  1466 AA.
AC   Q98TR8;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Cystic fibrosis transmembrane conductance regulator.
GN   CFTR.
OS   Bufo bufo (European toad).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Bufonidae; Bufo.
OX   NCBI_TaxID=8384;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BELLY SKIN;
RA   Amstrup J., Hviid Larsen E.;
RT   "Cloning of CFTR from Bufo bufo, Linnaeus, 1758.";
RL   Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY026761; AAK07685.1; -.
DR   HSSP; P13569; 1NBD.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR001140; ABCtranprtrTM.
DR   InterPro; IPR003439; ABC_transportr.
DR   InterPro; IPR005291; cAMP_cl_channel.
DR   Pfam; PF00664; ABC_membrane; 2.
DR   Pfam; PF00005; ABC_tran; 2.
DR   ProDom; PD000006; ABC_transportr; 2.
DR   SMART; SM00382; AAA; 2.
DR   TIGRFAMs; TIGR00953; 3a01202; 1.
DR   TIGRFAMs; TIGR01271; CFTR_protein; 1.
DR   PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
KW   ATP-binding; Transmembrane.
SQ   SEQUENCE   1466 AA;  165697 MW;  EB692EC3C611C169 CRC64;

  Query Match             42.2%;  Score 46;  DB 13;  Length 1466;
  Best Local Similarity   60.0%;  Pred. No. 3e+02;
  Matches    9;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GIGKFLKKAKKFGKA 15
              | |:||:|||:  ||
Db        400 GFGEFLEKAKQSNKA 414


RESULT 12
Q9VSK5
ID   Q9VSK5      PRELIMINARY;      PRT;  1963 AA.
AC   Q9VSK5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
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DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   CG6964 protein.
GN   GUG OR CG6964.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BERKELEY;
RX   MEDLINE=20196006; PubMed=10731132;
RA   Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA   Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA   George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA   Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA   Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA   Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA   Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA   Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA   Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA   Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA   Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA   de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA   Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA   Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA   Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA   Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA   Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA   Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA   Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA   Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA   Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA   Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA   Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA   Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA   Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA   Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA   Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA   Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA   Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA   Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA   Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA   Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA   Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA   Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA   Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT   "The genome sequence of Drosophila melanogaster.";
RL   Science 287:2185-2195(2000).
CC   -!- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
CC   -!- SIMILARITY: CONTAINS 1 MYB-LIKE DOMAIN.
DR   EMBL; AE003555; AAF50413.1; -.
DR   FlyBase; FBgn0020427; Gug.
DR   InterPro; IPR002951; Atrophin.
DR   InterPro; IPR001005; Myb_DNA_binding.
DR   Pfam; PF03154; Atrophin-1; 1.
DR   Pfam; PF00249; myb_DNA-binding; 1.
DR   SMART; SM00395; SANT; 1.
KW   DNA-binding; Nuclear protein.
SQ   SEQUENCE   1963 AA;  207927 MW;  8F386DE56E66CB68 CRC64;

  Query Match             42.2%;  Score 46;  DB 5;  Length 1963;
  Best Local Similarity   50.0%;  Pred. No. 3.9e+02;
  Matches    9;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 KFLKKAKKFGKAFVKILK 21
              ||:|  ::||| | :| |
Db        113 KFIKGLRQFGKNFFRIHK 130


RESULT 13
Q9NHX6
ID   Q9NHX6      PRELIMINARY;      PRT;  1966 AA.
AC   Q9NHX6;
DT   01-OCT-2000 (TrEMBLrel. 15, Created)
DT   01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   GRUNGE.
GN   GUG OR CG6964.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Erkner A., Roure A., Core N., Angelats C., Vola C., Fasano L.,
RA   Kerridge S.;
RT   "Grunge is required for proximal and ventral leg development in
RT   Drosophila.";
RL   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF217844; AAF34752.1; -.
DR   FlyBase; FBgn0020427; Gug.
DR   InterPro; IPR002951; Atrophin.
DR   InterPro; IPR001005; Myb_DNA_binding.
DR   Pfam; PF03154; Atrophin-1; 2.
DR   Pfam; PF00249; myb_DNA-binding; 1.
DR   SMART; SM00395; SANT; 1.
SQ   SEQUENCE   1966 AA;  208033 MW;  96AF90E2082E770C CRC64;

  Query Match             42.2%;  Score 46;  DB 5;  Length 1966;
  Best Local Similarity   50.0%;  Pred. No. 3.9e+02;
  Matches    9;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 KFLKKAKKFGKAFVKILK 21
              ||:|  ::||| | :| |
Db        134 KFIKGLRQFGKNFFRIHK 151


RESULT 14
Q8T9N4
ID   Q8T9N4      PRELIMINARY;      PRT;  1985 AA.
AC   Q8T9N4;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE   Transcriptional corepressor Atro.
GN   ATRO.
OS   Drosophila melanogaster (Fruit fly).
OC   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC   Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC   Ephydroidea; Drosophilidae; Drosophila.
OX   NCBI_TaxID=7227;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21652534; PubMed=11792320;
RA   Zhang S., Xu L., Lee J., Xu T.;
RT   "Drosophila atrophin homolog functions as a transcriptional
RT   corepressor in multiple developmental processes.";
RL   Cell 108:45-56(2002).
DR   EMBL; AF475087; AAL78679.1; -.
SQ   SEQUENCE   1985 AA;  210423 MW;  120A78F66C8FD67F CRC64;

  Query Match             42.2%;  Score 46;  DB 5;  Length 1985;
  Best Local Similarity   50.0%;  Pred. No. 4e+02;
  Matches    9;  Conservative    4;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          4 KFLKKAKKFGKAFVKILK 21
              ||:|  ::||| | :| |
Db        134 KFIKGLRQFGKNFFRIHK 151


RESULT 15
O97239
ID   O97239      PRELIMINARY;      PRT;  3933 AA.
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AC   O97239;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   Hypothetical 467.9 kDa protein.
GN   PFC0245C, MAL3P2.18.
OS   Plasmodium falciparum (isolate 3D7).
OC   Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX   NCBI_TaxID=36329;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=3D7;
RX   MEDLINE=99376085; PubMed=10448855;
RA   Bowman S., Lawson D., Basham D., Brown D., Chillingworth T.,
RA   Churcher C.M., Craig A., Davies R.M, Devlin K., Feltwell T.,
RA   Gentles S., Gwilliam R., Hamlin N., Harris D., Holroyd S., Hornsby T.,
RA   Horrocks P., Jagels K., Jassal B., Kyes S., McLean J., Moule S.,
RA   Mungall K., Murphy L., Oliver K., Quail M.A., Rajandream M.-A.,
RA   Rutter S., Skelton J., Squares R., Squares S., Sulston J.E.,
RA   Whitehead S., Woodward J.R., Newbold C., Barrell B.G.;
RT   "The complete nucleotide sequence of chromosome 3 of Plasmodium
RT   falciparum .";
RL   Nature 400:532-538(1999).
DR   EMBL; AL034558; CAB39005.1; -.
DR   InterPro; IPR002048; EF-hand.
DR   PROSITE; PS00018; EF_HAND; UNKNOWN_1.
KW   Hypothetical protein.
SQ   SEQUENCE   3933 AA;  467876 MW;  5144A4604EE36933 CRC64;

  Query Match             41.7%;  Score 45.5;  DB 5;  Length 3933;
  Best Local Similarity   41.2%;  Pred. No. 9.1e+02;
  Matches   14;  Conservative    1;  Mismatches    4;  Indels   15;  Gaps    1;

Qy          4 KFLKKAKKFGKAF--------------VKILKK 22
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Db       1454 KILKKNKKFIKLFFDINYLYFFCDNMFCLKILKK 1487


Search completed: June 30, 2003, 16:08:44
Job time : 30 secs
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Mayes
09/904753

FILE 'REGISTRY' ENTERED AT 14:12:12 ON 01 JUL 2003
L3 24 S GIGKFLKKAKKFGKAFVKILKK/SQSP

FILE 'HCAPLUS' ENTERED AT 14:12:50 ON 01 JUL 2003
L4 29 S L3

L4 ANSWER 1 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2003:57926 HCAPLUS
DOCUMENT NUMBER: 138:126965
TITLE: Use of antimicrobial peptides as preservatives in ophthalmic preparations including solutions, emulsions, and suspensions
INVENTOR(S): Lyons, Robert T.
PATENT ASSIGNEE(S): Allergan, Inc., USA
SOURCE: PCT Int. Appl., 43 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2003006046	A1	20030123	WO 2002-US22238	20020711
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, SK, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2003092612	A1	20030515	US 2001-904753	20010713

PRIORITY APPLN. INFO.: US 2001-904753 A 20010713

AB Methods for preserving ophthalmic compns. are disclosed. In one embodiment, such compns. include a liq. medium and an antimicrobial component which is preferably substantially non-oxidative. Compns. which include a liq. medium and antimicrobial peptide magainins, present in an amt. effective as a preservative, are also disclosed. Preserved compns. useful for administering a therapeutic component to the eyes or caring for contact lenses are also included within the scope of the present invention.

IT **155709-76-5**
RL: PAC (Pharmacological activity); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antimicrobial peptides as preservatives in ophthalmic prepns.)

REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 2 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:778109 HCAPLUS
DOCUMENT NUMBER: 137:284374
TITLE: Short bioactive peptides and methods for their use

INVENTOR(S): Owen, Donald R.
PATENT ASSIGNEE(S): Helix Biomedix, Inc., USA
SOURCE: PCT Int. Appl., 133 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002079408	A2	20021010	WO 2002-US9534	20020328
WO 2002079408	A3	20021128		
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZM, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM				
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG				
US 2003083243	A1	20030501	US 2001-820053	20010328
US 2003109452	A1	20030612	US 2002-109171	20020328

PRIORITY APPLN. INFO.: US 2001-279505P P 20010328
US 2001-820053 A 20010328

AB Short bioactive peptides contg. phenylalanine, leucine, alanine, and lysine residues are disclosed. The peptides can be used in antibacterial, antifungal, anticancer, and other biol. applications.

IT **147664-63-9**
RL: PAC (Pharmacological activity); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(short bioactive peptides and methods for their use)

L4 ANSWER 3 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:353473 HCAPLUS
DOCUMENT NUMBER: 136:386400
TITLE: Antibacterial agents comprising conjugates of glycopeptides and peptidic membrane-associating elements
INVENTOR(S): Cooper, Matthew Allister; Betley, Jason Richard
PATENT ASSIGNEE(S): Cambridge University Technical Services Limited, UK; Adprotech Limited
SOURCE: PCT Int. Appl., 64 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

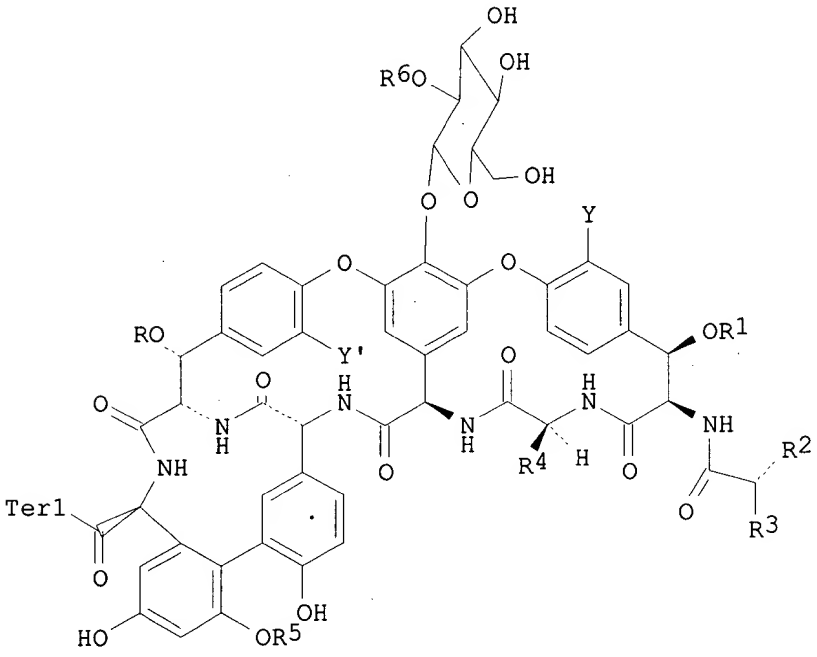
PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2002036612	A1	20020510	WO 2001-GB4867	20011102
W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ,				

LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ,
NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ,
TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY,
KG, KZ, MD, RU, TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH,
CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE,
TR, BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN,
TD, TG

AU 2002012482 A5 20020515 AU 2002-12482 20011102
PRIORITY APPLN. INFO.: GB 2000-26924 A 20001103
WO 2001-GB4867 W 20011102

OTHER SOURCE(S): MARPAT 136:386400

GI



I

AB Title antibacterial agents are derivs. of vancomycin-type antibiotics having structure V-L-W-X (V is a glycopeptide moiety which inhibits peptidoglycan biosynthesis in bacteria; L is a linking group; W is a peptidic membrane-assocg. element; X is H or a membrane-insertive element). V-L- has the structure I [Y, Y' = H, Cl; R = H, 4-epi-vancosaminyl, actinosaminyl, ristosaminyl, or a group -Ra-L-, where Ra is 4-epi-vancosaminyl, actinosaminyl, ristosaminyl and L is attached to the amino group of Ra; R1 = H or mannose; R2 = NH2, NHMe, NMe2, -NHL-, or -NMeL-; R3 = CH2CHMe2, [p-OH, m-Cl]phenyl, p-rhamnose-Ph, (p-rhamnose-galactose)phenyl, (p-galactose-galactose)phenyl, or [p-MeO-rhamnose]phenyl; R4 = CH2CONH2, benzyl, [p-OH]phenyl, or [p-OH, m-Cl]phenyl; R5 = H or mannose; R6 = H, 4-epi-vancosaminyl, vancosaminyl, actinosaminyl, ristosaminyl, or acosaminyl; or R6 is a group Rb-L-, where Rb is 4-epi-vancosaminyl, vancosaminyl, actinosaminyl, ristosaminyl or

acosaminyl and L is attached to the amino group of Rb; or R6 is a group Rb-R7, where R7 is an org. side chain moiety which is no more than 1000 Da]. Thus, N-(myristoyl)-Gly-Ser-Ser-Lys-Ser-Pro-Ser-Lys-Lys-Lys-Lys-Lys-Lys-Pro-Gly-Asp-(S-thioethyl-2-vancomycincarboxamide)-Cys-NH2 (PT2036), prepd. in 3 steps from vancomycin hydrochloride, showed min. inhibitory concns. 0.008, 0.008, and 0.004 mg/mL for E. faecium, E. faecalis, and S. aureus, resp.

IT **155709-76-5**
RL: PRP (Properties)
(unclaimed sequence; antibacterial agents comprising conjugates of glycopeptides and peptidic membrane-assocg. elements)

REFERENCE COUNT: 7 THERE ARE 7 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 4 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2002:131537 HCAPLUS
DOCUMENT NUMBER: 136:177951
TITLE: Biologically active peptides with reduced toxicity in animals and a method for preparing same
INVENTOR(S): Kari, U. Prasad; Williams, Taffy J.; McLane, Michael
PATENT ASSIGNEE(S): Magainin Pharmaceuticals, Inc., USA
SOURCE: U.S., 78 pp., Cont.-in-part of U.S. Ser. No. 893,006, abandoned.
CODEN: USXXAM
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 4
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
US 6348445	B1	20020219	US 1998-115737	19980715
US 5654274	A	19970805	US 1995-404283	19950314
US 5686563	A	19971111	US 1995-465325	19950605

PRIORITY APPLN. INFO.:
US 1992-891201 B2 19920601
US 1994-184462 B3 19940118
US 1995-465330 B2 19950605
US 1997-893006 B2 19970715

AB The present invention relates to biol. active peptides with reduced toxicity and methods of prepg. them. The peptides of the invention, which can be unsubstituted or N-terminal substituted have the formula: (T)(W)N-X, wherein X is a biol. active amphiphilic ion channel-forming peptide or protein, T is a lipophilic moiety or hydrogen, and W is T or hydrogen. Preferably T is: R(O)C-, wherein R is a hydrocarbon (alkyl or arom. or alkylarom.) having at least 2 and no more than 10 carbon atoms. T is preferably an octanoyl group. The peptides and proteins of the invention have improved antimicrobial and anti-tumor biol. activity while exhibiting reduced toxicity. A preferred method of reducing toxicity involves the formation of related methane sulfonate derivs. or analogs. Addnl., the compds. of the invention may be used to treat sepsis, septic shock, and lung infections, such as those occurring in cystic fibrosis.

IT **399524-28-8 399524-29-9**

RL: ADV (Adverse effect, including toxicity); PAC (Pharmacological activity); PKT (Pharmacokinetics); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antimicrobial and antitumor peptides with reduced toxicity in animals and a method for prepg. them)
REFERENCE COUNT: 45 THERE ARE 45 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 5 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:648594 HCAPLUS
DOCUMENT NUMBER: 136:324097
TITLE: A simple method for the purification of an antimicrobial peptide in recombinant Escherichia coli
AUTHOR(S): Hwang, Sung-Wook; Lee, Jae-Hyun; Park, Heung-Bok; Pyo, Sang-Hyun; So, Jin-Eon; Lee, Hyun-Soo; Hong, Seung-Suh; Kim, Jin-Hyun
CORPORATE SOURCE: Department of Chemical Engineering, Kongju National University, Kongju, 314-701, S. Korea
SOURCE: Molecular Biotechnology (2001), 18(3), 193-198
CODEN: MLBOEO; ISSN: 1073-6085
PUBLISHER: Humana Press Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A magainin deriv., designated MSI-344, was produced in Escherichia coli as fusion protein, by utilizing a truncated amidophoribosyltransferase of E. coli as a fusion partner. Bacterial cells transformed with the gene encoding the fusion protein were grown to a high cell d. and induced with isopropyl-1-thio-.beta.-D-galactoside (IPTG) to initiate product expression. The fusion protein was accumulated into cytoplasmic inclusion body and recombinant MSI-344 was released from the fusion partner by hydroxylamine treatment. Following cleavage of the fusion protein with hydroxylamine, the released MSI-344 was purified to homogeneity by cationic exchange chromatog. The final purity was at least 95% by reversed-phase high performance liq. chromatog. (RP-HPLC). Purified recombinant MSI-344 was found to be indistinguishable from the synthetic peptide detd. by amino acid sequences and antimicrobial activity assay.
IT **155709-76-5P**, MSI-344
RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); PUR (Purification or recovery); BIOL (Biological study); PREP (Preparation)
(simple method for purifn. of antimicrobial peptide in recombinant Escherichia coli)
IT **155709-76-5DP**, MSI-344, fusion protein with truncated Escherichia coli amidophosphoribosyltransferase
RL: BMF (Bioindustrial manufacture); BPN (Biosynthetic preparation); RCT (Reactant); BIOL (Biological study); PREP (Preparation); RACT (Reactant or reagent)
(simple method for purifn. of antimicrobial peptide in recombinant Escherichia coli)
REFERENCE COUNT: 20 THERE ARE 20 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 6 OF 29 HCAPLUS COPYRIGHT 2003 ACS

ACCESSION NUMBER: 2001:371097 HCAPLUS
DOCUMENT NUMBER: 134:365804
TITLE: Optimization of the hydroxylamine cleavage of an expressed fusion protein to produce a recombinant antimicrobial peptide
AUTHOR(S): Park, Heung-Bok; Pyo, Sang-Hyun; Hong, Seung-Suh; Kim, Jin-Hyun
CORPORATE SOURCE: Samyang Genex Biotech Research Institute, Taejeon, 305-348, S. Korea
SOURCE: Biotechnology Letters (2001), 23(8), 637-641
CODEN: BILED3; ISSN: 0141-5492
PUBLISHER: Kluwer Academic Publishers
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Hydroxylamine was used to cleave the Asn-Gly peptide bond between the fusion partner and the antimicrobial peptide of interest, a magainin deriv. (MSI-344). The efficiency of reaction depended on the hydroxylamine concn., denaturant, pH, and the fused protein concn. The optimal cleavage soln. consisted of guanidine.cntdot.HCl as the denaturant, pH 8.1, and 6.7 mg ml-1 of fused MSI-344. This optimized cleavage soln. resulted in a high yield (.apprx.95%) of MSI-344 from a cultivation of Escherichia coli. This result suggests potential applications for using hydroxylamine to cleave basic peptides produced from fusion proteins.

IT **155709-76-5P**, MSI-344
RL: BPN (Biosynthetic preparation); BIOL (Biological study); PREP (Preparation)
(optimization of hydroxylamine cleavage of expressed fusion protein to produce recombinant antimicrobial peptide)

REFERENCE COUNT: 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 7 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:338762 HCAPLUS
DOCUMENT NUMBER: 134:362292
TITLE: Methods of determining individual hypersensitivity to a pharmaceutical agent from gene expression profile
INVENTOR(S): Farr, Spencer
PATENT ASSIGNEE(S): Phase-1 Molecular Toxicology, USA
SOURCE: PCT Int. Appl., 222 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2001032928	A2	20010510	WO 2000-US30474	20001103
WO 2001032928	A3	20020725		

W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU,

TJ, TM
RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRIORITY APPLN. INFO.: US 1999-165398P P 19991105
US 2000-196571P P 20000411

AB The invention discloses methods, gene databases, gene arrays, protein arrays, and devices that may be used to det. the hypersensitivity of individuals to a given agent, such as drug or other chem., in order to prevent toxic side effects. In one embodiment, methods of identifying hypersensitivity in a subject by obtaining a gene expression profile of multiple genes assocd. with hypersensitivity of the subject suspected to be hypersensitive, and identifying in the gene expression profile of the subject a pattern of gene expression of the genes assocd. with hypersensitivity are disclosed. The gene expression profile of the subject may be compared with the gene expression profile of a normal individual and a hypersensitive individual. The gene expression profile of the subject that is obtained may comprise a profile of levels of mRNA or cDNA. The gene expression profile may be obtained by using an array of nucleic acid probes for the plurality of genes assocd. with hypersensitivity. The expression of the genes predetd. to be assocd. with hypersensitivity is directly related to prevention or repair of toxic damage at the tissue, organ or system level. Gene databases arrays and app. useful for identifying hypersensitivity in a subject are also disclosed.

IT **172820-23-4**, Pexiganan acetate
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(methods of detg. individual hypersensitivity to a pharmaceutical agent from gene expression profile)

L4 ANSWER 8 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2001:93819 HCAPLUS
DOCUMENT NUMBER: 135:101775
TITLE: The commercial development of the antimicrobial peptide pexiganan
AUTHOR(S): Zasloff, Michael
CORPORATE SOURCE: Magainin Pharmaceuticals Inc., PA, 19462, USA
SOURCE: Development of Novel Antimicrobial Agents: Emerging Strategies (2001), 261-270. Editor(s): Lohner, Karl. Horizon Scientific Press: Wymondham, UK.
CODEN: 69AXXR
DOCUMENT TYPE: Conference; General Review
LANGUAGE: English

AB A review with 24 refs. The development of an antimicrobial peptide from its discovery to its realization as a therapeutic is the subject of this personal account. The story spans at least 12 yr and has involved the efforts of hundreds of people, including both scientists and business people, involving disciplines ranging from peptide chem. to banking, at a cost of about $100,000,000. As yet the antimicrobial peptide remains unavailable for human therapeutic applications.

IT **147664-63-9P**, Pexiganan
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); SPN (Synthetic

preparation); BIOL (Biological study); PREP (Preparation)
(com. development of the antimicrobial peptide pexiganan)
REFERENCE COUNT: 8 THERE ARE 8 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 9 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:774985 HCAPLUS
DOCUMENT NUMBER: 135:29593
TITLE: High-Level Expression of Antimicrobial Peptide Mediated by a Fusion Partner Reinforcing Formation of Inclusion Bodies
AUTHOR(S): Lee, J. H.; Kim, J. H.; Hwang, S. W.; Lee, W. J.; Yoon, H. K.; Lee, H. S.; Hong, S. S.
CORPORATE SOURCE: Samyang Genex Biotech Research Institute, Yusung-gu, Taejon, 305-348, S. Korea
SOURCE: Biochemical and Biophysical Research Communications (2000), 277(3), 575-580
CODEN: BBRCA9; ISSN: 0006-291X
PUBLISHER: Academic Press
DOCUMENT TYPE: Journal
LANGUAGE: English
AB A gene expression system for antimicrobial peptides, which could be effectively used for various studies or applications of the antimicrobial peptides, has been developed. To avoid the harmful effects on an expression host, Escherichia coli, the antimicrobial peptides were expressed as fusion proteins with a polypeptide F4, which is a truncated PurF fragment that highly tends to form inclusion bodies. Seven different kinds of antimicrobial peptides have been successfully expressed by this expression system and the resulting expression level of fusion proteins reached up to 30% of total cell proteins. To confirm the identity of the recombinant peptide, MSI-344 was selected as a model peptide and purified to homogeneity, and we could obtain the recombinant MSI-344 of a high purity and with a good yield, which was identical to the authentic peptide in the aspects of the chem. and antimicrobial properties. These results show that the neutral fusion partner, which reinforces the formation of inclusion bodies, could mediate a high-level expression of the antimicrobial peptides. (c) 2000 Academic Press.
IT **155709-76-5P**, MSI-344
RL: BAC (Biological activity or effector, except adverse); BPN (Biosynthetic preparation); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study); PREP (Preparation)
(gene expression system for antimicrobial peptides, system demonstrated by producing functional recombinant MSI-344 peptides)
REFERENCE COUNT: 31 THERE ARE 31 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 10 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:401855 HCAPLUS
DOCUMENT NUMBER: 133:28274
TITLE: Method of separating basic peptide or basic protein from fusion protein using hydroxylamine
INVENTOR(S): Park, Heung-Bok; Pyo, Sang-Hyun; Hwang, Sung Wook; So, Jin-Eon; Kim, Jin-Hyun; Kim, Jeong Hyun; Hong, Seung-Suh; Lee, Hyun-Soo

PATENT ASSIGNEE(S): Samyang Genex Corporation, S. Korea
SOURCE: PCT Int. Appl., 18 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000034312	A1	20000615	WO 1999-KR748	19991208
W: AU, CA, CN, JP, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
KR 2000048051	A	20000725	KR 1999-56378	19991210

PRIORITY APPLN. INFO.: KR 1998-54566 A 19981210

AB The present invention relates to a method of recovering basic peptide or basic protein at a high yield from a fusion protein that has a hydroxylamine cleavage site between the basic peptide or basic protein and the fusion partner. More particularly, the present invention is composed of the processes of reacting fusion protein with hydroxylamine at a pH of 7.5 ~ 8.5 and recovering the basic peptide from the reaction mixt. Magainin deriv. MSI-344 was prepd. as a fusion peptide. The fusion product was purified from the culture medium. Then MSI-344 was cleaved using 6M hydroxylamine HCl at pH 8.1.

IT **155709-76-5P**
RL: BPN (Biosynthetic preparation); PEP (Physical, engineering or chemical process); PUR (Purification or recovery); BIOL (Biological study); PREP (Preparation); PROC (Process)
(method of sepg. basic peptide or basic protein from fusion protein using hydroxylamine)

REFERENCE COUNT: 6 THERE ARE 6 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 11 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 2000:207984 HCAPLUS
DOCUMENT NUMBER: 133:79160
TITLE: Oxidation of the N-terminal Gly-residue of peptides: stress study of pexiganan acetate in a drug formulation
AUTHOR(S): Feibush, Binyamin; Snyder, Bradley C.
CORPORATE SOURCE: Magainin Pharmaceuticals, Inc., Plymouth Meeting, PA, 19462, USA
SOURCE: Pharmaceutical Research (2000), 17(2), 197-204
CODEN: PHREEB; ISSN: 0724-8741
PUBLISHER: Kluwer Academic/Plenum Publishers
DOCUMENT TYPE: Journal
LANGUAGE: English

AB The purpose of this study was to identify four major degrdn. products, which were formed during a stress study of pexiganan (a 22-mer peptide) in a 1% formulation. The degrdn. products were isolated and characterized by LC/MS, tryptic and aminopeptidase digests. One of the degrdn. products was shown to be des-Gly1-pexiganan. The other three are structural isomers of N-glyoxylyl-desGly1-pexiganan. These isomers undergo reversible inter-conversions, as well as decomp. irreversibly to

des-Gly1-pexiganan. Thus, all the impurities were formed from a single oxidn. product of pexiganan, N-glyoxylyl-des-gly1-pexiganan. The aldehyde group of the glyoxylyl residue and the NH-amide of the adjacent isoleucine residue form a piperazinedione deriv. of des-gly1-pexiganan. This heterocyclic compd. rearranges to other tautomers or back to the N-glyoxylyl compd. Tryptic digests of the three degrdn. products showed that their N-terminal segment produced N-glyoxylyl-1-G-K whereas the N-terminal segment of pexiganan produced G-I-G-K. All the other tryptic-digest segments were identical to those formed in pexiganan. The LC/MS of the N-terminal segment and of synthetic N-glyoxylyl-I-G-K were identical. The enzymic resistance of the three impurities to undergo aminopeptidase-M cleavage further supported the conclusion that their N-terminal amino residues are substituted. After a year under stress conditions 1% pexiganan cream lost about 15% of the active component to oxidative-deamination, where the N-terminal glycine residue was oxidized to N-glyoxylyl-des-gly1-pexiganan. The other nine .epsilon.-amino lysine-residues of the peptide stayed intact. This oxidn. product inter-converted and formed two addnl. impurities, tautomers of piperazinedionyl-des-Gly1-pexiganan, and decompd. to des-Gly1-pexiganan, the forth impurity.

IT **147664-63-9**, Pexiganan **172820-23-4**, Pexiganan acetate
RL: PRP (Properties); RCT (Reactant); THU (Therapeutic use); BIOL (Biological study); RACT (Reactant or reagent); USES (Uses)
(oxidn. of the N-terminal Gly-residue in stress study of pexiganan acetate in a drug formulation)

REFERENCE COUNT: 15 THERE ARE 15 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 12 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:811265 HCAPLUS
DOCUMENT NUMBER: 132:50252
TITLE: Non-enzymic process for preparation of peptide C-terminal amides
INVENTOR(S): Jones, Stephen R.; Noecker, Lincoln A.; Feibush, Binyamin
PATENT ASSIGNEE(S): Magainin Pharmaceuticals, Inc., USA
SOURCE: PCT Int. Appl., 36 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9965931	A1	19991223	WO 1999-US13626	19990617
W: AU, CA, JP, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
CA 2331330	AA	19991223	CA 1999-2331330	19990617
AU 9946887	A1	20000105	AU 1999-46887	19990617
EP 1086121	A1	20010328	EP 1999-930329	19990617
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				

PRIORITY APPLN. INFO.: US 1998-89635P P 19980617

WO 1999-US13626 W 19990617

OTHER SOURCE(S): MARPAT 132:50252

AB A non-enzymic method of prepg. a peptide C-terminal amide comprises the steps of: reacting a peptide C-terminal carboxylic acid ester with an N-amino or N-oxy amide deriv. to form the corresponding peptide C-terminal N-amino or N-oxy amide deriv., which is converted to the corresponding C-terminal amide. The method was applied to the conversion of the peptide MSI-344 (GIGKFLKKAKKFGKAFVKILKK) to the C-terminal amide.

IT **155709-76-5**, Msi-344
RL: RCT (Reactant); RACT (Reactant or reagent)
(non-enzymic process for prepn. of peptide C-terminal amides)

IT **252741-87-0P 252741-89-2P**, MSI 1918
252741-90-5P 252856-51-2P, MSI 1922
RL: RCT (Reactant); SPN (Synthetic preparation); PREP (Preparation); RACT (Reactant or reagent)
(non-enzymic process for prepn. of peptide C-terminal amides)

IT **147664-63-9P 252741-92-7P**
RL: SPN (Synthetic preparation); PREP (Preparation)
(non-enzymic process for prepn. of peptide C-terminal amides)

REFERENCE COUNT: 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 13 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:795978 HCAPLUS
DOCUMENT NUMBER: 132:49114
TITLE: Manufacture of an antimicrobial peptide in Escherichia coli as a fusion protein with the purF gene products
INVENTOR(S): Kim, Jeong Hyun; Kang, Min Hyung; Lee, Jae-Hyun; Park, Se Ho; Lee, Joo Won; Hong, Seung Suh; Lee, Hyun-Soo
PATENT ASSIGNEE(S): Samyang Genex Corporation, S. Korea
SOURCE: PCT Int. Appl., 67 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 1
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9964611	A1	19991216	WO 1999-KR282	19990608
W: AU, CA, CN, JP, US				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
KR 2000005683	A	20000125	KR 1999-17920	19990514
CA 2301044	AA	19991216	CA 1999-2301044	19990608
AU 9941708	A1	19991230	AU 1999-41708	19990608
AU 754821	B2	20021128		
EP 1002107	A1	20000524	EP 1999-925435	19990608
R: DE, FR, GB, IT				
JP 2002517254	T2	20020618	JP 2000-553601	19990608

PRIORITY APPLN. INFO.:
KR 1998-22117 A 19980609
KR 1999-17920 A 19990514
WO 1999-KR282 W 19990608

AB A method of effective prodn. of an antimicrobial peptide by manuf.

as a fusion protein with the purF gene product (glutamine phosphoribosylpyrophosphate amidotransferase) is described. The fusion gene encodes a protein that has an antimicrobial peptide as the N-terminal moiety linked by a peptide contg. proteinase or chem. cleavage sites to all or part of the purF gene products. The fusion gene is terminated with the dual termination codon sequence TAATGA. By transforming E. coli with the expression vectors, the fusion gene under the control of T7 or lacZ promoter was expressed efficiently as a polypeptide which was cleavable to release antimicrobial peptide after purifn. In this way, the antimicrobial peptide can be expressed in E. coli with minimal toxicity and resistant to proteinase degrdn. The tested antimicrobial peptides included frog MSI-344 gene coded protein, and various frog or insects or human or carb peptides with the expression levels in the range of 4% to 35% of E. coli total proteins. The expression level of MSI-344 gene from the vector carrying 4 copies of the fusion genes (tetramer) was increased to 30% to 40% or 20% to 25% resp. in T7 and lacZ promoter constructs compared to that from the vector carring only a one copy of the fusion gene (monomer). The effective expression of these antimicrobial peptides in E. coli showed the potential of economical mass prodn. of the antimicrobial peptide for therapeutic use.

IT **155709-76-5DP**, MSI 344, fusion products with glutamine phosphoribosylpyrophosphate amidotransferase
RL: BPN (Biosynthetic preparation); PUR (Purification or recovery); RCT (Reactant); BIOL (Biological study); PREP (Preparation); RACT (Reactant or reagent)
(manuf. of antimicrobial peptide in Escherichia coli as fusion protein with purF gene products)

IT **155709-76-5 157414-20-5**
RL: PRP (Properties)
(unclaimed sequence; manuf. of an antimicrobial peptide in Escherichia coli as a fusion protein with the purF gene products)

REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 14 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:641320 HCAPLUS
DOCUMENT NUMBER: 132:18471
TITLE: Antiviral effects of synthetic membrane-active peptides on Herpes Simplex Virus, Type 1
AUTHOR(S): Egal, M.; Conrad, M.; MacDonald, D. L.; Maloy, W. L.; Motley, M.; Genco, C. A.
CORPORATE SOURCE: Department of Microbiology and Immunology, Morehouse School of Medicine, Atlanta, GA, USA
SOURCE: International Journal of Antimicrobial Agents (1999), 13(1), 57-60
CODEN: IAAGEA; ISSN: 0924-8579
PUBLISHER: Elsevier Science Ireland Ltd.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Magainins are cationic peptides with antimicrobial activity which were originally isolated from the skin of the African clawed frog (Xenopus laevis). Several synthetic derivs. of this class of peptides were evaluated for antiviral activity against herpes simplex virus, type 1 (HSV). Some of the peptides (MSI-102, -248, -420, -499/500 combination, -591, -594, and -1251) showed significant redn. of HSV plaque-forming units. The antiviral effect

was enhanced when HSV was pretreated with the peptides prior to inoculation onto Vero monolayers, suggesting a direct effect on the virion. Most of the peptides with anti-HSV activity were lysine-rich, and the addn. of octanoyl groups to the peptides appeared to enhance the antiviral effect.

IT **251940-85-9**, MSI 124
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antiviral effects of synthetic membrane-active peptides on herpes simplex virus type 1)

REFERENCE COUNT: 17 THERE ARE 17 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 15 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:623537 HCAPLUS
DOCUMENT NUMBER: 132:47394
TITLE: In vitro susceptibility to pexiganan of bacteria isolated from infected diabetic foot ulcers
AUTHOR(S): Ge, Y.; MacDonald, D.; Henry, M. M.; Hait, H. I.; Nelson, K. A.; Lipsky, B. A.; Zasloff, M. A.; Holroyd, K. J.
CORPORATE SOURCE: Magainin Pharmaceuticals Inc., Plymouth Meeting, PA, USA
SOURCE: Diagnostic Microbiology and Infectious Disease (1999), 35(1), 45-53
CODEN: DMIDDZ; ISSN: 0732-8893
PUBLISHER: Elsevier Science Inc.
DOCUMENT TYPE: Journal
LANGUAGE: English

AB During two clin. trials involving the treatment of 835 outpatients with infected diabetic foot ulcers, 2515 bacterial isolates, including 2337 aerobes and 178 anaerobes, were grown from cultures of the ulcers. The in vitro susceptibility of these isolates was detd. to pexiganan, a peptide anti-infective evaluated in these clin. trials, and to other classes of antibiotics. Pexiganan demonstrated broad spectrum antimicrobial activity against Gram-pos. and Gram-neg. aerobes and anaerobes. The MIC90 values for the most common species among 1735 Gram-pos. aerobes isolated, such as Staphylococcus aureus, coagulase-neg. staphylococci, Group A streptococci, and Group B streptococci, were 16 .mu.g/mL or less. Of 602 Gram-neg. aerobes tested, the MIC90 values for pexiganan were 16 .mu.g/mL or less for Acinetobacter, Pseudomonas, Stenotrophomonas, Citrobacter, Enterobacter, Escherichia, Klebsiella, and Flavobacterium species. Pexiganan had a MIC90 of 4 to 16 .mu.g/mL against the anaerobic isolates of Bacteroides, Peptostreptococcus, Clostridium, and Prevotella species. Importantly, pexiganan did not exhibit cross-resistance with other commonly used antibiotics, including .beta.-lactams, quinolones, macrolides, and lincosamides. The broad spectrum in vitro antimicrobial activity of pexiganan against clin. isolates from infected diabetic foot ulcers supports its potential as a local therapy for infected diabetic foot ulcers.

IT **147664-63-9**, Pexiganan
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)

(in vitro susceptibility to pexiganan of bacteria isolated from infected diabetic foot ulcers)
REFERENCE COUNT: 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 16 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:578829 HCAPLUS
DOCUMENT NUMBER: 132:137701
TITLE: Process impurity identification in MSI-78
AUTHOR(S): Chang, J. L.; Bai, J.; Jiang, J.; Pilgrim, R.; Chang, W.-S.; Kollie, T. O.; Rasmussen, R.; Tews, E.; Miller, R. B.; Tolle, J. C.
CORPORATE SOURCE: Abbott Laboratories, North Chicago, IL, 60064, USA
SOURCE: Peptide Science: Present and Future, Proceedings of the International Peptide Symposium, 1st, Kyoto, Nov. 30-Dec. 5, 1997 (1999), Meeting Date 1997, 569-570. Editor(s): Shimonishi, Yasutsugu. Kluwer: Dordrecht, Neth. CODEN: 68BYA5
DOCUMENT TYPE: Conference
LANGUAGE: English
AB A symposium on identification of process impurities in peptide MSI-78, for use in treatment of infection in diabetic foot ulcers.
IT **172820-23-4P**
RL: SPN (Synthetic preparation); PREP (Preparation)
(identification of process impurities in the large-scale prodn. of MSI-78)
REFERENCE COUNT: 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 17 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:240386 HCAPLUS
DOCUMENT NUMBER: 131:29715
TITLE: In vitro antibacterial properties of pexiganan, an analog of magainin
AUTHOR(S): Ge, Yigong; Macdonald, Dorothy L.; Holroyd, Kenneth J.; Thornsberry, Clyde; Wexler, Hannah; Zasloff, Michael
CORPORATE SOURCE: Magainin Pharmaceuticals Inc., Plymouth Meeting, PA, 19462, USA
SOURCE: Antimicrobial Agents and Chemotherapy (1999), 43(4), 782-788
CODEN: AMACCQ; ISSN: 0066-4804
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Pexiganan, a 22-amino-acid antimicrobial peptide, is an analog of the magainin peptides isolated from the skin of the African clawed frog. Pexiganan exhibited in vitro broad-spectrum antibacterial activity when it was tested against 3,109 clin. isolates of Gram-pos. and Ggram-neg., anaerobic and aerobic bacteria. The pexiganan MIC at which 90% of isolates are inhibited (MIC90) was 32 .mu.g/mL or less for Staphylococcus spp., Streptococcus spp., Enterococcus faecium, Corynebacterium spp., Pseudomonas spp., Acinetobacter spp., Stenotrophomonas spp., certain species of the

family Enterobacteriaceae, Bacteroides spp., Peptostreptococcus spp., and Propionibacterium spp. Comparison of the MICs and min. bactericidal concns. (MBCs) of pexiganan for 143 isolates representing 32 species demonstrated that for 92% of the isolates tested, MBCs were the same or within 1 twofold difference of the MICs, consistent with a bactericidal mechanism of action. Killing curve anal. showed that pexiganan killed Pseudomonas aeruginosa rapidly, with 106 organisms/mL eliminated within 20 min of treatment with 16 .mu.g of pexiganan per mL. No evidence of cross-resistance to a no. of other antibiotic classes was obsd., as detd. by the equivalence of the MIC50s and the MIC90s of pexiganan for strains resistant to oxacillin, cefazolin, cefoxitin, imipenem, ofloxacin, ciprofloxacin, gentamicin, and clindamycin vs. those for strains susceptible to these antimicrobial agents. Attempts to generate resistance in several bacterial species through repeated passage with subinhibitory concns. of pexiganan were unsuccessful. In conclusion, pexiganan exhibits properties in vitro which make it an attractive candidate for development as a topical antimicrobial agent.

IT **147664-63-9**, Pexiganan
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(in vitro antibacterial properties of pexiganan)

REFERENCE COUNT: 27 THERE ARE 27 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 18 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:81582 HCAPLUS
DOCUMENT NUMBER: 130:134201
TITLE: Biologically active peptides with reduced toxicity in animals and a method for preparing same
INVENTOR(S): Kari, U. Prasad; Williams, Taffy J.; McLane, Michael
PATENT ASSIGNEE(S): Magainin Pharmaceuticals Inc., USA
SOURCE: PCT Int. Appl., 201 pp.
CODEN: PIXXD2
DOCUMENT TYPE: Patent
LANGUAGE: English
FAMILY ACC. NUM. COUNT: 4
PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 9903488	A2	19990128	WO 1998-US14610	19980715
WO 9903488	A3	19990408		
W: AU, CA, JP				
RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE				
AU 9883005	A1	19990210	AU 1998-83005	19980715
EP 1001800	A2	20000524	EP 1998-933343	19980715
R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI				
JP 2001510164	T2	20010731	JP 2000-502785	19980715

PRIORITY APPLN. INFO.: US 1997-893006 A 19970715
WO 1998-US14610 W 19980715
OTHER SOURCE(S): MARPAT 130:134201

AB Biol. active peptides with reduced toxicity, and methods of prepg. them, are provided. The peptides, which can be unsubstituted or N-terminal substituted, have formula (T)(W)NX (X = biol. active amphiphilic ion channel-forming peptide or protein; T = H, lipophilic moiety; W = H, T). Preferably T is RC(O) (R = C2-10 alkyl or arom. or alkylarom.). T is preferably an octanoyl group. The peptides and proteins of the invention have improved antimicrobial and anti-tumor biol. activity while exhibiting reduced toxicity. A preferred method of reducing toxicity involves the formation of related methane sulfonate derivs. or analogs. Addnl., the compds. of the invention may be used to treat sepsis, septic shock, and lung infections, such as those occurring in cystic fibrosis.

IT **147664-63-9DP**, methane sulfonate derivs.
155709-76-5DP, methane sulfonate derivs.
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses)
(peptide inhibition of lipopolysaccharide binding to hydrophobic dye)

IT **147664-63-9 155709-76-5**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(peptide inhibition of lipopolysaccharide binding to hydrophobic dye)

L4 ANSWER 19 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:62895 HCAPLUS
DOCUMENT NUMBER: 130:293828
TITLE: Biological activities of 1,1,6-trisubstituted indanes: beyond magainin 2
AUTHOR(S): Numao, Naganori; Hirota, Yukiko; Iwahori, Akiyo; Kidokoro, Shun-Ichi; Sasatsu, Masanori; Kondo, Isamu; Itoh, Sachiko; Itoh, Etsuko; Katoh, Tadashi; Shimozono, Noriko; Yamazaki, Akiko; Takao, Ken-Ichi; Bobayashi, Susumu
CORPORATE SOURCE: Sagami Chemical Research Center, Kanagawa, 229-0012, Japan
SOURCE: Biological & Pharmaceutical Bulletin (1999), 22(1), 73-76
CODEN: BPBLEO; ISSN: 0918-6158
PUBLISHER: Pharmaceutical Society of Japan
DOCUMENT TYPE: Journal
LANGUAGE: English
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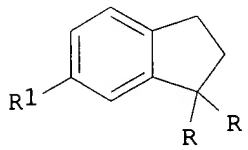

I R=$(CH_2)_4NH_2$, R^1=benzyl
II R=benzyl, R^1=$(CH_2)_4NH_2$

Searcher : Shears 308-4994

AB MSI-78 is a peptide analog of naturally occurring magainin 2 isolated from the skin of Xenopus laevis. The peptide is known to have one of the strongest antibacterial activities in magainin 2 analogs against methicillin-resistant Staphylococcus aureus (MRSA). To find novel compds. superior to MSI-78, we have further designed and synthesized 1,1-di(4-aminobutyl)-6-benzylindane (PM4, I) and 1,1-dibenzyl-6-(4-aminobutyl) indane (PM5, II) and tested their inhibitory ability on the growth of S. aureus. In an in vitro assay, I showed the same antibacterial activity against the bacterium as MSI-78, and non-hemolytic activity against human red blood cells (RBCs) at the MIC (min. inhibitory concn.) value, in contrast to the latter. On the other hand, although II showed stronger antibacterial activity than MSI-78, it showed hemolytic activity at the MIC value. Otherwise, stronger decarboxylase activity for oxaloacetate was obsd. for II, but not for I.

IT **172820-23-4**, MSI 78
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(biol. activities of indane trisubstituted derivs. compared with some other peptidomimetics and magainin 2 analogs)

REFERENCE COUNT: 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 20 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1999:42084 HCAPLUS
DOCUMENT NUMBER: 130:217491
TITLE: Pexiganan acetate
AUTHOR(S): Lamb, Harriet M.; Wiseman, Lynda R.
CORPORATE SOURCE: Adis International Limited, Auckland, N. Z.
SOURCE: Drugs (1998), 56(6), 1047-1052
CODEN: DRUGAY; ISSN: 0012-6667
PUBLISHER: Adis International Ltd.
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English

AB A review with 19 refs. Pexiganan acetate (MSI 78) is a synthetic cationic peptide (22 amino acids) with antibacterial activity. It is an analog of magainin 2, which is a host defense peptide isolated from frog skin. The drug is thought to act by disturbing the permeability of the cell membrane or cell wall. Pexiganan acetate has good in vitro activity against Gram-pos. and Gram-neg. aerobes; 99% of strains were susceptible to the agent using a break-point of 64 mg/L. Eighty-nine to 97% of anaerobes were susceptible to pexiganan acetate using the same break-point. After 7 passages in vitro, there was no evidence of resistance to pexiganan acetate among 2 strains of Staphylococcus aureus. In 2 phase III multicenter randomized double-blind trials in diabetic patients with infected foot ulcers, both topical pexiganan acetate 1% and oral ofloxacin 800 mg/day achieved clin. cure or improvement in about 90% of patients. Eradication of pathogens in the 2 studies was achieved in 82% of ofloxacin recipients and 66% of pexiganan acetate recipients at the end of therapy. Limited data indicate that pexiganan acetate is well tolerated.

IT **172820-23-4**, Pexiganan acetate
RL: BAC (Biological activity or effector, except adverse); BPR (Biological process); BSU (Biological study, unclassified); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES

(Uses)
(antibacterial and pharmacokinetics of pexiganan acetate in humans)
REFERENCE COUNT: 19 THERE ARE 19 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 21 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1998:360054 HCAPLUS
DOCUMENT NUMBER: 129:130749
TITLE: Pexiganan acetate (Cytolex; MSI-78): topical antimicrobial
AUTHOR(S): Graul, A.; Leeson, P.
CORPORATE SOURCE: Prous Science, Barcelona, 08080, Spain
SOURCE: Drugs of the Future (1998), 23(3), 271-273
CODEN: DRFUD4; ISSN: 0377-8282
PUBLISHER: Prous Science
DOCUMENT TYPE: Journal; General Review
LANGUAGE: English
AB A review, with 16 refs., describing the pharmacol. and clin. properties of the topical antimicrobial pexiganan acetate, a 22-amino-acid synthetic analog of the naturally occurring peptide magainin 2.
IT **172820-23-4**, Pexiganan acetate
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses)
(antimicrobial pharmacol. of)
REFERENCE COUNT: 18 THERE ARE 18 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 22 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1998:271688 HCAPLUS
DOCUMENT NUMBER: 129:38663
TITLE: In vitro antimicrobial activity of MSI-78, a magainin analog
AUTHOR(S): Fuchs, Peter C.; Barry, Arthur L.; Brown, Steven D.
CORPORATE SOURCE: The Clinical Microbiology Institute, Wilsonville, OR, 97070, USA
SOURCE: Antimicrobial Agents and Chemotherapy (1998), 42(5), 1213-1216
CODEN: AMACCQ; ISSN: 0066-4804
PUBLISHER: American Society for Microbiology
DOCUMENT TYPE: Journal
LANGUAGE: English
AB MSI-78 is a cationic peptide with broad-spectrum antimicrobial activity and has been developed as a topical agent. The authors compared the in vitro activity of MSI-78 with those of ofloxacin and other antibiotics against fresh clin. isolates. Based on MIC distribution statistics, strains for which the MSI-78 MIC was .ltoreq.64 .mu.g/mL were assumed to be susceptible for purposes of this report. Of 411 aerobic isolates tested, 91% were susceptible to MSI-78, compared to 91% for ofloxacin and 92% for ciprofloxacin. Only enterococci consistently required .gtoreq.64 .mu.g of MSI-78/mL for inhibition. MSI-78 demonstrated bactericidal activity equiv. to that of ofloxacin. Of 61 anaerobes, 97% were susceptible to MSI-78.

Of 10 isolates of Candida albicans, 3 were inhibited by MSI-78 at 24 h. Further studies of this compd. appear to be warranted.

IT **172820-23-4**, MSI 78
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(in vitro antibacterial activity of magainin analog MSI-78)

REFERENCE COUNT: 11 THERE ARE 11 CITED REFERENCES AVAILABLE FOR THIS RECORD. ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 23 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1997:478371 HCAPLUS
DOCUMENT NUMBER: 127:202749
TITLE: On the antibacterial activity of normal and reversed magainin 2 analogs against Helicobacter pylori
AUTHOR(S): Iwahori, Akiyo; Hirota, Yukiko; Sampe, Ruriko; Miyano, Sanae; Takahashi, Noriko; Sasatsu, Masanori; Kondo, Isamu; Numao, Naganori
CORPORATE SOURCE: Sagami Chemical Research Center, Sagamihara, 229, Japan
SOURCE: Biological & Pharmaceutical Bulletin (1997), 20(7), 805-808
CODEN: BPBLEO; ISSN: 0918-6158
PUBLISHER: Pharmaceutical Society of Japan
DOCUMENT TYPE: Journal
LANGUAGE: English

AB Magainin 2 is an antimicrobial peptide isolated from the skin of Xenopus laevis. The antibacterial activities of normal and reversed magainin 2 analogs were tested against 2 strains of H. pylori (ATCC 43526, ATCC 43579), compared with those against Escherichia coli (ATCC 25922) and Staphylococcus aureus (ATCC 25923). Among these analogs, MSI-78A showed the strongest activity against H. pylori. The MIC (min. inhibitory concn.) values were almost the same as those against E. coli and S. aureus. No or lesser activity was obsd. in all the reversed peptides compared to the corresponding normal magainin 2 analogs. Based on the CD measurement, the more active peptide tends to show a higher .alpha.-content. The pos.-charged 5 amino acids (KILKK) positioned at the C terminus on the amphipathic .alpha.-helical structure play important roles in exerting the strong activity against H. pylori. This indicates that the net charge of the cell surface in H. pylori may be more neg. than that of E. coli, though both strains belong to the same genus.

IT **147664-63-9**
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); BIOL (Biological study)
(antibacterial activity of normal and reversed magainin 2 analogs against Helicobacter pylori)

L4 ANSWER 24 OF 29 HCAPLUS COPYRIGHT 2003 ACS
ACCESSION NUMBER: 1997:478370 HCAPLUS
DOCUMENT NUMBER: 127:185405
TITLE: Antibacterial activity of two alkylamines integrated an indane scaffold: mimicry of a complementary unit on magainin 2
AUTHOR(S): Numao, Naganori; Iwahori, Akiyo; Hirota, Yukiko; Sasatsu, Masanori; Kondo, Isamu; Onimura, Kenjiro; Sampe, Ruriko; Yamane, Shinji; Itoh,

Sachiko; Katoh, Tadashi; Kobayashi, Susumu
CORPORATE SOURCE: Sagami Chemical Research Center, Sagamihara, 229, Japan
SOURCE: Biological & Pharmaceutical Bulletin (1997), 20(7), 800-804
CODEN: BPBLEO; ISSN: 0918-6158
PUBLISHER: Pharmaceutical Society of Japan
DOCUMENT TYPE: Journal
LANGUAGE: English
AB Based on the antibacterial activity of 9-phenylnonylamine (pC9a) against Escherichia coli (ATCC29522) and Staphylococcus aureus (ATCC25923), we have further tested the inhibitory ability of the growth of the bacteria by (.+-.)1-(4-aminobutyl)-6-benzylindane (PM2) and (.+-.)1-benzyl-6-(4-aminobutyl) indane (PM3), i.e., two kinds of 1,6-disubstituted indanes. In an in vitro assay, they showed almost the same antibacterial activities against the bacteria as pC9a, as well as that of magainin 2 analogs (i.e., the peptides MSI-78 and 87-ISM), except in the case of 87-ISM against S. aureus. At the MIC (min. inhibitory concn.) values, however, their killing rate of E. coli is actually quicker than pC9a. This indicates that an indane scaffold, used as a template to mimic a part of the .alpha.-helical structure of magainin 2, can accelerate the killing rate. At present, however, it is unknown whether either the hydrophobicity or the .alpha.-helical structure, or both, of the indane scaffold is involved in accelerating the rate. Moreover, these two indanes also showed stronger antibacterial activity against two strains of Helicobacter pylori (ATCC43526, ATCC43579) than either pC9a or magainin 2 related peptides.
IT **172820-23-4**, MSI 78
RL: BAC (Biological activity or effector, except adverse); BSU (Biological study, unclassified); PRP (Properties); BIOL (Biological study)
(antibacterial activity of two alkylamines integrated an indane scaffold: mimicry of a complementary unit on magainin 2)

E1 THROUGH E24 ASSIGNED

FILE 'REGISTRY' ENTERED AT 14:13:20 ON 01 JUL 2003
L5 24 SEA FILE=REGISTRY ABB=ON PLU=ON (155709-76-5/BI OR 147664-63-9/BI OR 172820-23-4/BI OR 157414-20-5/BI OR 155709-77-6/BI OR 157414-17-0/BI OR 157414-18-1/BI OR 157414-19-2/BI OR 157414-21-6/BI OR 157414-22-7/BI OR 157414-23-8/BI OR 157414-35-2/BI OR 157414-36-3/BI OR 157414-37-4/BI OR 157414-38-5/BI OR 157414-39-6/BI OR 251940-85-9/BI OR 252741-87-0/BI OR 252741-89-2/BI OR 252741-90-5/BI OR 252741-92-7/BI OR 252856-51-2/BI OR 399524-28-8/BI OR 399524-29-9/BI)

L6 24 L5 AND L3

L6 ANSWER 1 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **399524-29-9** REGISTRY
CN L-Lysine, glycyl-L-isoleucylglycyl-L-lysyl-L-phenylalanyl-L-leucyl-L-lysyl-L-lysyl-L-alanyl-L-lysyl-L-lysyl-L-phenylalanylglycyl-L-lysyl-L-alanyl-L-phenylalanyl-L-valyl-L-lysyl-L-isoleucyl-L-leucyl-L-lysyl-, monomethanesulfonate, monosodium salt (9CI) (CA INDEX NAME)
SQL 22

SEQ 1 GIGKFLKKAK KFGKAFVKIL KK
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HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

SEQ 1 GIGKFLKKAK KFGKAFVKIL KK
========== ========== ==
HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

SEQ 1 GIGKFLKKAK KFGKAFVKIL KK
========== ========== ==
HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:177951

L6 ANSWER 2 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **399524-28-8** REGISTRY
CN L-Lysinamide, glycyl-L-isoleucylglycyl-L-lysyl-L-phenylalanyl-L-leucyl-L-lysyl-L-lysyl-L-alanyl-L-lysyl-L-lysyl-L-phenylalanylglycyl-L-lysyl-L-alanyl-L-phenylalanyl-L-valyl-L-lysyl-L-isoleucyl-L-leucyl-L-lysyl-, monomethanesulfonate, monosodium salt (9CI) (CA INDEX NAME)
SQL 22

SEQ 1 GIGKFLKKAK KFGKAFVKIL KK
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HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

SEQ 1 GIGKFLKKAK KFGKAFVKIL KK
========== ========== ==

HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

SEQ 1 GIGKFLKKAK KFGKAFVKIL KK
========== ========== ==
HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 136:177951

L6 ANSWER 3 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **252856-51-2** REGISTRY
CN Protein MSI 1922 (synthetic) (9CI) (CA INDEX NAME)
CI MAN
SQL 67

SEQ 1 MKAIFVLLEH HHHHLKDAQT NSSSNNNNNN NNNNLGIEGR ISEFNGIGKF
=====

51 LKKAKKFGKA FVKILKK
========== =======
HITS AT: 46-67

REFERENCE 1: 132:50252

L6 ANSWER 4 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **252741-92-7** REGISTRY
CN L-Lysinamide, glycyl-L-isoleucylglycyl-L-lysyl-L-phenylalanyl-L-leucyl-L-lysyl-L-lysyl-L-alanyl-L-lysyl-L-lysyl-L-phenylalanylglycyl-L-lysyl-L-alanyl-L-phenylalanyl-L-valyl-L-lysyl-L-isoleucyl-L-leucyl-L-lysyl-, mono(trifluoroacetate) (9CI) (CA INDEX NAME)
SQL 22

SEQ 1 GIGKFLKKAK KFGKAFVKIL KK
========== ========== ==
HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

SEQ 1 GIGKFLKKAK KFGKAFVKIL KK
========== ========== ==
HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

SEQ 1 GIGKFLKKAK KFGKAFVKIL KK
========== ========== ==
HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 132:50252

L6 ANSWER 5 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **252741-90-5** REGISTRY
CN L-Lysinamide, glycyl-L-isoleucylglycyl-L-lysyl-L-phenylalanyl-L-leucyl-L-lysyl-L-lysyl-L-alanyl-L-lysyl-L-lysyl-L-phenylalanylglycyl-

L-lysyl-L-alanyl-L-phenylalanyl-L-valyl-L-lysyl-L-isoleucyl-L-leucyl-L-lysyl-N-hydroxy-, mono(trifluoroacetate) (salt) (9CI) (CA INDEX NAME)
SQL 22

SEQ 1 GIGKFLKKAK KFGKAFVKIL KK
========== ========== ==
HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

SEQ 1 GIGKFLKKAK KFGKAFVKIL KK
========== ========== ==
HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

SEQ 1 GIGKFLKKAK KFGKAFVKIL KK
========== ========== ==
HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 132:50252

L6 ANSWER 6 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **252741-89-2** REGISTRY
CN L-Lysinamide, glycyl-L-isoleucylglycyl-L-lysyl-L-phenylalanyl-L-leucyl-L-lysyl-L-lysyl-L-alanyl-L-lysyl-L-lysyl-L-phenylalanylglycyl-L-lysyl-L-alanyl-L-phenylalanyl-L-valyl-L-lysyl-L-isoleucyl-L-leucyl-L-lysyl-N-hydroxy- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN MSI 1918
CI COM
SQL 22

SEQ 1 GIGKFLKKAK KFGKAFVKIL KK
========== ========== ==
HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 132:50252

L6 ANSWER 7 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **252741-87-0** REGISTRY
CN L-Lysine, glycyl-L-isoleucylglycyl-L-lysyl-L-phenylalanyl-L-leucyl-L-lysyl-L-lysyl-L-alanyl-L-lysyl-L-lysyl-L-phenylalanylglycyl-L-lysyl-L-alanyl-L-phenylalanyl-L-valyl-L-lysyl-L-isoleucyl-L-leucyl-L-lysyl-, methyl ester (9CI) (CA INDEX NAME)
SQL 22

SEQ 1 GIGKFLKKAK KFGKAFVKIL KK
========== ========== ==
HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 132:50252

L6 ANSWER 8 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **251940-85-9** REGISTRY
CN D-Lysinamide, glycyl-D-isoleucylglycyl-D-lysyl-D-phenylalanyl-D-leucyl-D-lysyl-D-lysyl-D-alanyl-D-lysyl-D-lysyl-D-phenylalanylglycyl-D-lysyl-D-alanyl-D-phenylalanyl-D-valyl-D-lysyl-D-isoleucyl-D-leucyl-D-lysyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN MSI 124
SQL 22

SEQ 1 GIGKFLKKAK KFGKAFVKIL KK
========== ========== ==
HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 132:18471

L6 ANSWER 9 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **172820-23-4** REGISTRY
CN L-Lysinamide, glycyl-L-isoleucylglycyl-L-lysyl-L-phenylalanyl-L-leucyl-L-lysyl-L-lysyl-L-alanyl-L-lysyl-L-lysyl-L-phenylalanylglycyl-L-lysyl-L-alanyl-L-phenylalanyl-L-valyl-L-lysyl-L-isoleucyl-L-leucyl-L-lysyl-, acetate (9CI) (CA INDEX NAME)
OTHER NAMES:
CN Cytolex
CN MSI 78
CN Pexiganan acetate
SQL 22

SEQ 1 GIGKFLKKAK KFGKAFVKIL KK
========== ========== ==
HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

SEQ 1 GIGKFLKKAK KFGKAFVKIL KK
========== ========== ==
HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

SEQ 1 GIGKFLKKAK KFGKAFVKIL KK
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HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 134:362292

REFERENCE 2: 133:79160

REFERENCE 3: 132:137701

REFERENCE 4: 130:293828

REFERENCE 5: 130:217491

REFERENCE 6: 129:130749

REFERENCE 7: 129:38663

REFERENCE 8: 127:185405

L6 ANSWER 10 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **157414-39-6** REGISTRY
CN Magainin I, N-acetyl-7-L-lysine-8-L-lysine-10-L-lysine-18-L-lysine-19-de-L-glutamic acid-21-L-leucine-23-L-lysine-23a-L-aspartic acid-23b-L-aspartic acid-23c-L-lysinamide- (9CI) (CA INDEX NAME)
SQL 25

SEQ 1 GIGKFLKKAK KFGKAFVKIL KKDDK
========== ========== ==
HITS AT: 1-22

REFERENCE 1: 121:170579

L6 ANSWER 11 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **157414-38-5** REGISTRY
CN Magainin I, N-[N2-(N2-acetyl-L-arginyl)-L-arginyl]-7-L-lysine-8-L-lysine-10-L-lysine-18-L-lysine-19-de-L-glutamic acid-21-L-leucine-23-L-lysinamide- (9CI) (CA INDEX NAME)
SQL 24

SEQ 1 RRGIGKFLKK AKKFGKAFVK ILKK
======== ========== ====
HITS AT: 3-24

REFERENCE 1: 121:170579

L6 ANSWER 12 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **157414-37-4** REGISTRY
CN Magainin I, N-(N-acetyl-L-methionyl)-7-L-lysine-8-L-lysine-10-L-lysine-18-L-lysine-19-de-L-glutamic acid-21-L-leucine-23-L-lysinamide- (9CI) (CA INDEX NAME)
SQL 23

SEQ 1 MGIGKFLKKA KKFGKAFVKI LKK
========= ========== ===
HITS AT: 2-23

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 121:170579

L6 ANSWER 13 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **157414-36-3** REGISTRY
CN Magainin I, N-acetyl-7-L-lysine-8-L-lysine-10-L-lysine-18-L-lysine-19-de-L-glutamic acid-21-L-leucine-23-L-lysine-23a-L-aspartamide- (9CI) (CA INDEX NAME)
SQL 23

SEQ 1 GIGKFLKKAK KFGKAFVKIL KKN
========== ========== ==

HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 121:170579

L6 ANSWER 14 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **157414-35-2** REGISTRY
CN Magainin I, N-acetyl-7-L-lysine-8-L-lysine-10-L-lysine-18-L-lysine-19-de-L-glutamic acid-21-L-leucine-23-L-lysine-23a-L-argininamide- (9CI) (CA INDEX NAME)
SQL 23

SEQ 1 GIGKFLKKAK KFGKAFVKIL KKR
========== ========== ==
HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 121:170579

L6 ANSWER 15 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **157414-23-8** REGISTRY
CN Magainin I, N-(N2-L-arginyl-L-arginyl)-7-L-lysine-8-L-lysine-10-L-lysine-18-L-lysine-19-de-L-glutamic acid-21-L-leucine-23-L-lysine-23a-glycine- (9CI) (CA INDEX NAME)
SQL 25

SEQ 1 RRGIGKFLKK AKKFGKAFVK ILKKG
======== ========== ====
HITS AT: 3-24

REFERENCE 1: 121:170579

L6 ANSWER 16 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **157414-22-7** REGISTRY
CN Magainin I, N-(N-L-methionyl-L-methionyl)-7-L-lysine-8-L-lysine-10-L-lysine-18-L-lysine-19-de-L-glutamic acid-21-L-leucine-23-L-lysine-23a-glycine- (9CI) (CA INDEX NAME)
SQL 25

SEQ 1 MMGIGKFLKK AKKFGKAFVK ILKKG
======== ========== ====
HITS AT: 3-24

REFERENCE 1: 121:170579

L6 ANSWER 17 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **157414-21-6** REGISTRY
CN Magainin I, N-L-arginyl-7-L-lysine-8-L-lysine-10-L-lysine-18-L-lysine-19-de-L-glutamic acid-21-L-leucine-23-L-lysine- (9CI) (CA INDEX NAME)
SQL 23

SEQ 1 RGIGKFLKKA KKFGKAFVKI LKK
========= ========== ===
HITS AT: 2-23

REFERENCE 1: 121:170579

L6 ANSWER 18 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **157414-20-5** REGISTRY
CN L-Lysine, L-methionylglycyl-L-isoleucylglycyl-L-lysyl-L-phenylalanyl-L-leucyl-L-lysyl-L-lysyl-L-alanyl-L-lysyl-L-lysyl-L-phenylalanylglycyl-L-lysyl-L-alanyl-L-phenylalanyl-L-valyl-L-lysyl-L-isoleucyl-L-leucyl-L-lysyl- (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Magainin I, N-L-methionyl-7-L-lysine-8-L-lysine-10-L-lysine-18-L-lysine-19-de-L-glutamic acid-21-L-leucine-23-L-lysine-
OTHER NAMES:
CN 81: PN: WO9964611 FIGURE: 1 unclaimed sequence
SQL 23

SEQ 1 MGIGKFLKKA KKFGKAFVKI LKK
========= ========== ===
HITS AT: 2-23

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 132:49114

REFERENCE 2: 121:170579

L6 ANSWER 19 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **157414-19-2** REGISTRY
CN Magainin I, 7-L-lysine-8-L-lysine-10-L-lysine-18-L-lysine-19-de-L-glutamic acid-21-L-leucine-23-L-lysine-23a-L-asparagine- (9CI) (CA INDEX NAME)
SQL 23

SEQ 1 GIGKFLKKAK KFGKAFVKIL KKN
========== ========== ==
HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 121:170579

L6 ANSWER 20 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **157414-18-1** REGISTRY
CN Magainin I, 7-L-lysine-8-L-lysine-10-L-lysine-18-L-lysine-19-de-L-glutamic acid-21-L-leucine-23-L-lysine-23a-L-homoserine- (9CI) (CA INDEX NAME)
SQL 23

SEQ 1 GIGKFLKKAK KFGKAFVKIL KKX
========== ========== ==
HITS AT: 1-22

REFERENCE 1: 121:170579

L6 ANSWER 21 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **157414-17-0** REGISTRY
CN Magainin I, 7-L-lysine-8-L-lysine-10-L-lysine-18-L-lysine-19-de-L-glutamic acid-21-L-leucine-23-L-lysine-23a-L-arginine- (9CI) (CA INDEX NAME)

SQL 23

SEQ 1 GIGKFLKKAK KFGKAFVKIL KKR
========== ========== ==
HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 121:170579

L6 ANSWER 22 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **155709-77-6** REGISTRY
CN Magainin I, 7-L-lysine-8-L-lysine-10-L-lysine-18-L-lysine-19-de-L-glutamic acid-21-L-leucine-23-L-lysine-23a-glycine- (9CI) (CA INDEX NAME)
SQL 23

SEQ 1 GIGKFLKKAK KFGKAFVKIL KKG
========== ========== ==
HITS AT: 1-22

REFERENCE 1: 121:4511

L6 ANSWER 23 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **155709-76-5** REGISTRY
CN L-Lysine, glycyl-L-isoleucylglycyl-L-lysyl-L-phenylalanyl-L-leucyl-L-lysyl-L-lysyl-L-alanyl-L-lysyl-L-lysyl-L-phenylalanylglycyl-L-lysyl-L-alanyl-L-phenylalanyl-L-valyl-L-lysyl-L-isoleucyl-L-leucyl-L-lysyl- (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Magainin I, 7-L-lysine-8-L-lysine-10-L-lysine-18-L-lysine-19-de-L-glutamic acid-21-L-leucine-23-L-lysine-
OTHER NAMES:
CN 1: PN: WO03006046 SEQID: 1 claimed protein
CN 23: PN: WO0236612 SEQID: 31 unclaimed sequence
CN 82: PN: WO9964611 FIGURE: 1 unclaimed sequence
CN MSI 344
CI COM
SQL 22

SEQ 1 GIGKFLKKAK KFGKAFVKIL KK
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HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 138:126965

REFERENCE 2: 136:386400

REFERENCE 3: 136:324097

REFERENCE 4: 135:29593

REFERENCE 5: 134:365804

REFERENCE 6: 133:28274

REFERENCE 7: 132:50252

REFERENCE 8: 132:49114

REFERENCE 9: 130:134201

REFERENCE 10: 124:334852

L6 ANSWER 24 OF 24 REGISTRY COPYRIGHT 2003 ACS
RN **147664-63-9** REGISTRY
CN L-Lysinamide, glycyl-L-isoleucylglycyl-L-lysyl-L-phenylalanyl-L-leucyl-L-lysyl-L-lysyl-L-alanyl-L-lysyl-L-lysyl-L-phenylalanylglycyl-L-lysyl-L-alanyl-L-phenylalanyl-L-valyl-L-lysyl-L-isoleucyl-L-leucyl-L-lysyl- (9CI) (CA INDEX NAME)
OTHER CA INDEX NAMES:
CN Magainin I, 7-L-lysine-8-L-lysine-10-L-lysine-18-L-lysine-19-de-L-glutamic acid-21-L-leucine-23-L-lysinamide-
OTHER NAMES:
CN Pexiganan
CI COM
SQL 22

SEQ 1 GIGKFLKKAK KFGKAFVKIL KK
========== ========== ==
HITS AT: 1-22

RELATED SEQUENCES AVAILABLE WITH SEQLINK

REFERENCE 1: 137:284374

FERENCE 2: 135:101775

REFERENCE 3: 133:79160

REFERENCE 4: 132:50252

REFERENCE 5: 132:47394

REFERENCE 6: 131:29715

REFERENCE 7: 130:134201

REFERENCE 8: 127:202749

REFERENCE 9: 126:293604

REFERENCE 10: 119:63022

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